

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1642GXN

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * Welcome to STN International * * * * * * * * *

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 "Ask CAS" for self-help around the clock
NEWS 3 Jun 03 New e-mail delivery for search results now available
NEWS 4 Aug 08 PHARMAMarketLetter(PHARMAML) - new on STN
NEWS 5 Aug 19 Aquatic Toxicity Information Retrieval (AQUIRE)
now available on STN
NEWS 6 Aug 26 Sequence searching in REGISTRY enhanced
NEWS 7 Sep 03 JAPIO has been reloaded and enhanced
NEWS 8 Sep 16 Experimental properties added to the REGISTRY file
NEWS 9 Sep 16 CA Section Thesaurus available in CAPLUS and CA
NEWS 10 Oct 01 CASREACT Enriched with Reactions from 1907 to 1985
NEWS 11 Oct 24 BEILSTEIN adds new search fields
NEWS 12 Oct 24 Nutraceuticals International (NUTRACEUT) now available on STN
NEWS 13 Nov 18 DKILIT has been renamed APOLLIT
NEWS 14 Nov 25 More calculated properties added to REGISTRY
NEWS 15 Dec 04 CSA files on STN
NEWS 16 Dec 17 PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS 17 Dec 17 TOXCENTER enhanced with additional content
NEWS 18 Dec 17 Adis Clinical Trials Insight now available on STN
NEWS 19 Jan 29 Simultaneous left and right truncation added to COMPENDEX,
ENERGY, INSPEC
NEWS 20 Feb 13 CANCERLIT is no longer being updated
NEWS 21 Feb 24 METADEX enhancements
NEWS 22 Feb 24 PCTGEN now available on STN
NEWS 23 Feb 24 TEMA now available on STN
NEWS 24 Feb 26 NTIS now allows simultaneous left and right truncation
NEWS 25 Feb 26 PCTFULL now contains images
NEWS 26 Mar 04 SDI PACKAGE for monthly delivery of multifile SDI results
NEWS 27 Mar 20 EVENTLINE will be removed from STN
NEWS 28 Mar 24 PATDPAFULL now available on STN
NEWS 29 Mar 24 Additional information for trade-named substances without
structures available in REGISTRY
NEWS 30 Apr 11 Display formats in DGENE enhanced
NEWS 31 Apr 14 MEDLINE Reload
NEWS 32 Apr 17 Polymer searching in REGISTRY enhanced
NEWS 33 Jun 13 Indexing from 1947 to 1956 added to records in CA/CAPLUS
NEWS 34 Apr 21 New current-awareness alert (SDI) frequency in
WPIDS/WPINDEX/WPIX
NEWS 35 Apr 28 RDISCLOSURE now available on STN
NEWS 36 May 05 Pharmacokinetic information and systematic chemical names
added to PHAR
NEWS 37 May 15 MEDLINE file segment of TOXCENTER reloaded
NEWS 38 May 15 Supporter information for ENCOMPPAT and ENCOMPLIT updated
NEWS 39 May 16 CHEMREACT will be removed from STN
NEWS 40 May 19 Simultaneous left and right truncation added to WSCA
NEWS 41 May 19 RAPRA enhanced with new search field, simultaneous left and
right truncation
NEWS 42 Jun 06 Simultaneous left and right truncation added to CBNB

NEWS 43 Jun 06 PASCAL enhanced with additional data
NEWS 44 Jun 20 2003 edition of the FSTA Thesaurus is now available
NEWS 45 Jun 25 HSDB has been reloaded

NEWS EXPRESS April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT
MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
AND CURRENT DISCOVER FILE IS DATED 01 APRIL 2003
NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
NEWS PHONE Direct Dial and Telecommunication Network Access to STN
NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

All use of STN is subject to the provisions of the STN Customer agreement. Please note that this agreement limits use to scientific research. Use for software development or design or implementation of commercial gateways or other similar uses is prohibited and may result in loss of user privileges and other penalties.

* *

FILE 'HOME' ENTERED AT 15:05:12 ON 27 JUN 2003

=> file .gary	SINCE FILE	TOTAL
COST IN U.S. DOLLARS	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 15:05:17 ON 27 JUN 2003

FILE 'CANCERLIT' ENTERED AT 15:05:17 ON 27 JUN 2003

FILE 'BIOSIS' ENTERED AT 15:05:17 ON 27 JUN 2003
COPYRIGHT (C) 2003 BIOLOGICAL ABSTRACTS INC. (R)

FILE 'EMBASE' ENTERED AT 15:05:17 ON 27 JUN 2003
COPYRIGHT (C) 2003 Elsevier Science B.V. All rights reserved.

FILE 'SCISEARCH' ENTERED AT 15:05:17 ON 27 JUN 2003
COPYRIGHT 2003 THOMSON ISI

=> 59D8
59D8 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (>).

=> s 59D8
L1 117 59D8

=> s l1 and monoclonal
L2 89 L1 AND MONOCLONAL

=> s l2 and py<=1997
2 FILES SEARCHED...
4 FILES SEARCHED...
L3 83 L2 AND PY<=1997

=> s l3 and (cancer? or ?carcinoma or neoplas? or tumour? or tumor? or metast?)
2 FILES SEARCHED...
L4 2 L3 AND (CANCER? OR ?CARCINOMA OR NEOPLAS? OR TUMOUR? OR TUMOR?)

OR METAST?)

=> dup rem 14
PROCESSING COMPLETED FOR L4
L5 1 DUP REM L4 (1 DUPLICATE REMOVED)

=> d ibib abs

L5 ANSWER 1 OF 1 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 93190305 MEDLINE
DOCUMENT NUMBER: 93190305 PubMed ID: 8446952
TITLE: High-level expression of antibody-plasminogen activator fusion proteins in hybridoma cells.
AUTHOR: Love T W; Quertermous T; Zavodny P J; Runge M S; Chou C C; Mullins D; Huang P L; Schnee J M; Kestin A S; Savard C E; +
CORPORATE SOURCE: Massachusetts General Hospital, Boston 02114.
CONTRACT NUMBER: HL-02414 (NHLBI)
HL-19259 (NHLBI)
SOURCE: THROMBOSIS RESEARCH, (1993 Jan 15) 69 (2) 221-9.
Journal code: 0326377. ISSN: 0049-3848.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199304
ENTRY DATE: Entered STN: 19930416
Last Updated on STN: 19930416
Entered Medline: 19930408

AB We show that the mouse gamma 2b heavy chain or human beta-globin 3' untranslated region can greatly enhance protein expression in myeloma cells transfected by genes coding for antibody-plasminogen activator fusion proteins. Expression plasmids were constructed containing a cloned genomic heavy chain variable region from fibrin-specific monoclonal antibody 59D8, a cloned genomic constant region of the mouse gamma 2b heavy chain, and DNA sequence coding for either tissue-type plasminogen activator (tPA) or a segment of urokinase (UK) and their respective 3' untranslated sequences. Cell lines transfected with these constructs, pSVtPA (tPA) and pSVUKG(UK), produced extremely low levels of mRNA and protein (0.008-0.06 micrograms/ml) in comparison with the parental 59D8 myeloma cell line (7.6-10 micrograms/ml). In vitro nuclear run-off analysis indicated that the low steady-state levels of mRNA encoded by pSVUKG(UK) did not result from a lower rate of transcription of the transfected gene (relative to the rate of transcription of the endogenous heavy chain gene in the 59D8 parent cells). In an attempt to increase protein secretion, we assembled the expression plasmids pSVtPA(Ig), pSVUKG(Ig), and pSVUKG(beta), in which the 3' untranslated region of the mouse gamma 2b heavy chain or human beta-globin gene was substituted for the 3' untranslated region of the plasminogen activator gene. Analysis of supernatant media from cell lines transfected with these constructs showed an increase in recombinant protein secretion of 68 to 100 fold in comparison with that from cell lines transfected with pSVtPA(tPA) or pSVUKG(UK).

=> d his

(FILE 'HOME' ENTERED AT 15:05:12 ON 27 JUN 2003)

FILE 'MEDLINE, CANCERLIT, BIOSIS, EMBASE, SCISEARCH' ENTERED AT 15:05:17
ON 27 JUN 2003

L1 117 S 59D8
L2 89 S L1 AND MONOCLONAL
L3 83 S L2 AND PY<=1997
L4 2 S L3 AND (CANCER? OR ?CARCINOMA OR NEOPLAS? OR TUMOUR? OR TUMO

L5

1 DUP REM L4 (1 DUPLICATE REMOVED)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

on: June 16, 2003, 16:02:14 ; Search time 10.2667 Seconds
(without alignments)
20.061 Million cell updates/sec

Title:	US-09-424-940A-1
Effect score:	41
Sequence:	1 GHRPLDK 7
Scoring table:	BLOSUM62
Gapop:	10.0 , Gapext: 0.5
Searched:	265574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters:	262574
Minimum DB seq length:	0
Minimum DB seq length:	0
Post-processing:	Maximum Match 0% Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn_6/_picodata/1/iaa/5A_COMB.pep:**
2: /cgn_6/_picodata/1/iaa/5B_COMB.pep:**
3: /cgn_6/_picodata/1/iaa/6A_COMB.pep:**
4: /cgn_6/_picodata/1/iaa/6B_COMB.pep:**
5: /cgn_6/_picodata/1/iaa/PCUTS_COMB.pep:**
6: /cgn_6/_picodata/1/iaa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-424-940A-1
; Sequence 10, Application US/08058699
; Patent No. 5413827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marshall S. Range
; TITLE OF INVENTION: FIBRIN-TARGETTED INHIBITORS OF
; THROMBIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930303
; CLASSIFICATION: 530
; PRIORITY APPLICATION NUMBER: N/A
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; RECOMMENDATION NUMBER: 05433/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
; US-08-058-699-10

SUMMARIES

#	Query	Score	Match	Length	DB	ID	Description
1	41	100.0	7	1	US-08-699-10		Sequence 10, Appl
2	41	100.0	8	1	US-08-699-11		Sequence 11, Appl
3	41	100.0	10	2	US-08-448-547-1		Sequence 1, Appl
4	41	100.0	28	1	US-08-135-12		Sequence 12, Appl
5	41	100.0	28	1	US-08-470-152-12		Sequence 10, Appl
6	41	100.0	28	2	US-08-168-964B-10		Sequence 10, Appl
7	41	100.0	28	2	US-07-282B-10		Sequence 10, Appl
8	41	100.0	28	2	US-08-290-852-33		Sequence 33, Appl
9	41	100.0	28	2	US-08-553-678A-10		Sequence 10, Appl
10	41	100.0	28	3	US-08-382-134B-10		Sequence 10, Appl
11	41	100.0	28	3	US-08-170-299-10		Sequence 10, Appl
12	41	100.0	30	2	US-08-290-853-35		Sequence 35, Appl
13	41	100.0	31	1	US-08-472-535-9		Sequence 9, Appl
14	41	100.0	31	1	US-08-484-774-9		Sequence 9, Appl
15	41	100.0	31	3	US-08-286-170A-9		Sequence 9, Appl
16	41	100.0	491	1	US-08-206-176-4		Sequence 4, Appl
17	31	75.6	66	4	US-09-177-249-296		Sequence 296, Appl
18	31	75.6	170	1	US-08-227-372-1		Sequence 1, Appl
19	31	75.6	170	6	5194425-3		Patent No. 5194425
20	31	75.6	215	1	US-08-107-684B-9		Sequence 9, Appl
21	31	75.6	215	1	US-08-107-684B-13		Sequence 13, Appl
22	31	75.6	219	4	US-09-134-001C-4644		Sequence 4644, Appl
23	30	73.2	21	1	US-08-507-124-4		Sequence 4, Appl
24	30	73.2	117	4	US-09-199-637A-33		Sequence 33, Appl
25	30	73.2	253	4	US-09-180-109A-35		Sequence 35, Appl
26	30	73.2	254	2	US-09-180-823-19		Sequence 31, Appl
27	30	73.2	358	2	US-09-180-823-19		Sequence 19, Appl

Query Match Best Local Similarity 100.0% ; Score 41; DB 1; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
1 | | | | |
1 GHRPLDK 7

Db ; Sequence 11, Application US/08058699
; Patent No. 5443827

RESULT 2
US-08-058 699-11

GENERAL INFORMATION:
APPLICANT: Edgar Haber
APPLICANT: Christopher Bode
APPLICANT: Marshall S. Runge
TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF THROMBIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/058,699
FILING DATE: 19930503
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A

ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser, Ph.D.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: Linear

US-08-058-699-11

Query Match 100.0%; Score 41; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
1 | | | | |
1 GHRPLDK 7

Db ; Sequence 1, Application US/08448547
; Patent No. 5821068

RESULT 3
US-08-448-547-1

GENERAL INFORMATION:
APPLICANT: Soe, Gilbu
APPLICANT: Kohno, Isao
APPLICANT: Inuzuka, Kimiko
APPLICANT: Ito, Yumiko
TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY, AND IMMUNOASSAYING METHOD
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,547
FILING DATE: 30-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01844
FILING DATE: 01-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-297325
FILING DATE: 02-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-38931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-448-547-1

Query Match 100.0%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 4
US-08-486-135-12

GENERAL INFORMATION:
Patent No. 5720934
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-Jones, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for Imaging
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,135

FILING DATE: 06-JUN-1995
 CLASSIFICATION: 4.24
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 572093-nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,205-N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEX: 910-21-5317
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-486-135-12

Query Match Score 41; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.048;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 5
 US-08-470-152-12
 Sequence 12, Application US/08470152
 Patent No. 5780007
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 APPLICANT: Buttram, Scott
 APPLICANT: McBride, William
 APPLICANT: Lister-James, John
 APPLICANT: Civitello, Edgar R.
 TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Allegretti, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 STATE: IL
 CITY: Chicago
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,964B
 FILING DATE: 06-JUN-1995
 CLASIFICATION: 4.24
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniel, Patricia A.
 REGISTRATION NUMBER: 33,194
 REFERENCE/DOCKET NUMBER: DTRI 111D4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (603) 437-8970
 TELEFAX: (603) 437-8977
 INFORMATION FOR SEQ ID NO: 10:
 NUMBER OF SEQUENCES: 19
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-468-964B-10

Query Match Score 41; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.048;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 7
 US-07-871-282A-10
 Sequence 10, Application US/07871282A
 Patent No. 5965107
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 APPLICANT: Buttram, Scott
 APPLICANT: McBride, William
 APPLICANT: Lister-James, John
 APPLICANT: Civitello, Edgar R.
 TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Allegretti, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 STATE: IL
 CITY: Chicago
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,152
 FILING DATE: 06-JUN-1995
 CLASIFICATION: 4.24
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5700007-nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,205-L
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1234
 TELEX: 910-221-5317
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-470-152-12

Query Match Score 41; DB 1; Length 28;

TITLE OF INVENTION: Imaging
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Diatide, Inc.
 STREET: 9 Delta Drive
 CITY: Londonderry
 STATE: NH
 COUNTRY: USA
 ZIP: 03053

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/871,282A
 FILING DATE: 20-APR-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniel's, Patricia A.
 REGISTRATION NUMBER: 33,194
 REFERENCE/DOCKET NUMBER: DITI 1.11
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (603) 437-8970
 TELEFAX: (603) 437-8977
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 8
 US-08-290-853-33
 Query Match 100 %; Score 41; DB 2; Length 28;
 Best Local Similarity 100 %; Pred. No. 0.040; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 9
 US-08-253-678A-10
 Query Match 100 %; Score 41; DB 2; Length 28;
 Best Local Similarity 100 %; Pred. No. 0.048; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 9
 US-08-253-678A-10
 Sequence 10, Application US/08253678A
 Patent No. 5917844
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 ATTORNEY: McBride, William
 Lister-Jones, John
 CIVITELLO, Edgar R.
 TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
 NUMBER OF SEQUENCES: 23
 COUNTRY: USA
 ZIP: 03053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/253,678A
 FILING DATE: 03-JUN-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniel's, Patricia A.
 REGISTRATION NUMBER: 33,194
 REFERENCE/DOCKET NUMBER: DITI 112
 TELEPHONE: (603) 437-8970
 TELEFAX: (603) 437-8977
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid

TITLE OF INVENTION: Imaging Inflammation
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESS: Banner & Allegretti, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/290,853
 FILING DATE: 11-OCT-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5989519nan, Kevin E.
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,112-H

OTHER INFORMATION: residue is protected by an acetoamidomethyl
US-08-484-774-9

Query Match 100.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
Db 4 GHRPLDK 10

RESULT 15

US-08-266-178A-9

Sequence 9, Application US/08266178A

Patent No. 6017510

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Techneum-99m Labeled Peptides for

TITLE OF INVENTION: Imaging Inflammation

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/266,178A

FILING DATE: 27-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 6017510nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,112

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE: Modified site

NAME/KEY: Modified site

LOCATION: 1..3

OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= "The amino terminal residue is

OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine

OTHER INFORMATION: residue is protected by an acetoamidomethyl

US-08-266-178A-9

Query Match 100.0%; Score 41; DB 3; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7

Db 4 GHRPLDK 10

CC used to immunise mice. The mouse spleen cells and amyeloma cell
 CC line can be fused to produce a hybridoma secreting Mabs which bind
 CC specifically to human fibrin but not fibrinogen.
 XX

SQ Sequence 8 AA;
 Query Match 100.0%; Score 50; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS Synthetic.

Qy 1 GHRPLDKC 8
 |||||
 1 GHRPLDKC 8

Db

RESULT 2

AAR44837

ID AAR44837 standard; peptide; 8 AA.

XX

AC AAR44837;

XX

DT 20-JUN-1994 (first entry)

XX

DE Human fibrin beta-chain N-terminal peptide A.

XX

KW Tissue plasminogen activator; t-PA; mutain; fibrin; antigen;

KW anti-fibrin; monoclonal antibody; hybridoma; thrombolytic

KW anti-thrombotic agent; bispecific antibody.

XX

OS Synthetic.

XX

PN JP05304992-A.

XX

PD 19-NOV-1993.

XX

PF 17-JUN-1992; 92JP-0158301.

XX

PR 20-JUN-1991; 91JP-0148936.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

DR WPI: 1993-408334/51.

XX

Hybrid monoclonal antibody - used for prepn. of thrombolytic drug

PT having increased thrombolytic activity and specificity and

PT reduced reactivity to fibrinogen

PS Example 1: Page 14; 38pp; Japanese.

XX

CC Human fibrin beta-chain Peptides A and B were synthesised and coupled

CC to BSA for injection into mice. The peptides were used to raise

CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin

CC which also recognise truncated tPA muateins lacking the finger, EGF and

CC Kringle 1 domains.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 50; DB 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 |||||
 1 GHRPLDKC 8

Db

RESULT 3

AAR63270

ID AAR63270 standard; peptide; 8 AA.

XX

AC AAR63270;

XX

DE Fibrin-specific epitopic peptide.

DT 21-JUL-1995 (first entry)
 XX synthetic beta-peptide used to raise monoclonal antibody 59D8.
 DE KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
 XX KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
 KW coronary stent implantation; adjunctive therapy; fibrinogen;
 KW hemorrhage.
 XX OS Synthetic.

XX WO9425491-A.

PN

PD 10-NOV-1994.

XX PF 03-MAY-1994; 94WO-US04881.

PR 03-MAY-1991; 93US-0058699.

XX PA (HARD) HARVARD COLLEGE.
 PA (UYEM-) UNIV EMORY.

XX PI Bode C, Haber E, Runge M;

DR WPI: 1994-358195/44.

XX PT Fibrin-binding antibody linked to thrombin inhibitor - useful for
 PT preventing blood coagulation by specifically targetting inhibitor
 PT to site of thrombin activity

XX PS Example 1: Page 14; 53pp; English.

XX This sequence represents a synthetic beta-peptide which was used to
 CC immunopurify the monoclonal antibody 59D8 which was raised against
 CC beta Peptide (see also AAR63268). The antibody binds fibrin and may be
 CC used in the chimeric molecule of the invention. The chimeric molecule
 CC further comprises a thrombin inhibitor linked to the fibrin-binding
 CC antibody through a covalent linkage. The chimeric molecule allows
 CC fibrin-specific antibody targetting of hirudin and other thrombin
 CC inhibitors, which is more potent than thrombin on its own. The epitope
 CC to which 59D8 binds becomes available only after thrombin cleaves
 CC fibrinopeptide B. The chimeric protein may be used for preventing
 CC coagulation of the blood. Anti-thrombin targeting of the fibrin-binding
 CC antibody can be used as an adjunctive therapy with highly selective
 CC thrombolytic agents. The thrombin inhibitor is localised to sites
 CC of thrombin activity which binds to thrombin but does
 CC not cross react with uncleaved fibrinogen. The selectivity of
 CC inhibition allows the total amount of thrombin used to be
 CC substantially reduced, resulting in a reduced potential for generalised
 CC haemorrhaging.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 50; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 |||||
 1 GHRPLDKC 8

Db

XX AC AAR65793;

XX ID AAR65793 standard; peptide; 8 AA.

XX DT 26-JUN-1995 (first entry)

XX DE Fibrin-specific epitopic peptide.

KW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
KW antifibrin-specific monoclonal antibodies.

XX PD 22-OCT-1987.

OS PF 14-APR-1987; 87WO-US00862.

XX PF 14-APR-1986; 86US-0851514.

FH Key Location/Qualifiers

FT Misc-difference 8 /note= "May be absent and if present
may be bonded to keyhole limpet
hemocyanin."

XX PR (GEHO-) GEN HOSPITAL CORP.
(GENO-) GEN HOSPITAL CORP.

PA PT Matsueda GR, Haber E;

PN DR WPI; 1987-306855/43.

XX PT Screening of fibrin-specific monoclonal antibodies - by contact
with immobilised crosslinked fibrin clot and screening with
detectable labelling step

XX PR Disclosure; Page 7; 41PP; English.

XX PS The Mabs are specific to fibrin without fibrinogen cross-reactivity.

CC CC They have increased binding to in vitro and in vivo thrombi. The
Mabs can be used in immunoassays for fibrin in the presence of
fibrinogen or other proteins. They can be used as immunoaffinity
ligands for the purification of fibrin.

XX CC (Updated on 03-OCT-2002 to add missing OS field.)

DR XX Sequence 7 AA;

XX SQ Query Match 82.0%; Score 41; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

XX AC RESULT 6
ID AAR05558 standard; peptide; 7 AA.
XX XX
AC AAR05558;
XX DT 11-OCT-1990 (first entry)

CC CC AAR05558 are synthetic peptides comprising fibrin-specific
epitopic sequences, they can be used to prepare hybridoma cell
lines, which produce antifibrin-specific monoclonal antibodies
substantially devoid of fibrinogen cross-reactivity. These
antibodies are useful in the in vivo and in vitro detection
of thrombi and fibrin deposits.

XX PS Sequence 8 AA;

XX SQ Query Match 100.0%; Score 50; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
Db 1 GHRPLDKC 8

XX DE Peptide antigenic to fibrin.
XX KW fibrin; fibrinogen; thrombi; immunoaffinity.
XX OS Synthetic.

XX XX Key Location/Qualifiers

XX FT Misc-difference 2 /label=His or Pro

XX FT Misc-difference 4 /label=Pro or Val

XX FT Misc-difference 5 /label=Pro or Val

XX FT Misc-difference 6 /label=Leu or Val

XX FT Misc-difference 7 /label=Asp or Glu

XX FT Misc-difference 7 /label=Lys or Arg

XX PN US4927916-A.

XX PD 22-MAY-1990.

XX PP 30-JAN-1986; 86US-0824228.

FH Key Location/Qualifiers

FT Misc-difference 7 /label= Lys-OH

XX PR 23-APR-1984; 84US-0603155.
PR 30-JAN-1986; 86US-0824228.

PN WO8706263-A.

PA (GEHO-) GEN HOSPITAL CORP.
 XX Matsueda GR, Haber E, Hui K;
 PI WPI: 1990-185723/24.

XX DR
 PT Fibrin-specific monoclonal antibodies -
 PT lacking fibrinogen cross-reactivity, obt'd. using peptide(s)
 comprising fibrin-specific epitopic sequences.
 XX PS
 XX Claim 1; Page 17; 12pp; English.

CC Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be raised without cross-reactivity to fibrinogen. They are particularly useful in detection of fibrin and thrombi.
 CC Sequence 7 AA;

Query Match 82.0%; Score 41; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QQ 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 7
 ID AAR63269 standard; peptide; 7 AA.
 XX
 AC AAR63269;
 DE Beta-peptide used to raise monoclonal antibody 59D8.
 XX
 KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
 KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
 KW coronary stent implantation; adjunctive therapy; fibrinogen;
 KW haemorrhage.
 XX Synthetic.
 XX PN WO9425491-A.
 XX PD 10-NOV-1994.
 XX PF 03-MAY-1994; 94WO-US04881.
 XX PR 03-MAY-1993; 93US-0058699.
 XX PA (HARD) HARVARD COLLEGE.
 XX (UYEM-) UNIV EMORY.
 XX PI Bode C, Haber E, Runge M;
 XX DR WPI: 1994-358195/44.
 XX PT Fibrin-binding antibody linked to thrombin inhibitor - useful for preventing blood coagulation by specifically targetting inhibitor to site of thrombin activity
 XX
 PS Example 1; Page 13; 53pp; English.
 XX This sequence represents beta-peptide which was used to raise the monoclonal antibody 59D8. The antibody binds fibrin and may be used in the chimeric molecule of the invention. The chimeric molecule further comprises a thrombin inhibitor linked to the fibrin-binding antibody through a covalent linkage. The chimeric molecule allows fibrin-specific antibody targetting of hirudin and other thrombin inhibitors, which is more potent than thrombin on its own. The epitope to which 59D8 binds becomes available only after thrombin cleaves

CC fibrinopeptide B. The chimeric protein may be used for preventing coagulation of the blood. Anti-thrombin targetting can be esp. useful in highly thrombogenic situations such as coronary stent implantation and can be used as an adjunctive therapy with highly selective thrombolytic agents. The thrombin inhibitor is localised to sites of thrombin activity by the antibody which binds to thrombin but does not cross react with uncleaved fibrinogen. The selectivity of inhibition allows the total amount of thrombin inhibitor used to be substantially reduced, resulting in a reduced potential for generalised haemorrhaging.
 XX SQ Sequence 7 AA;

Query Match 82.0%; Score 41; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QQ 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 8
 ID AAR65792 standard; peptide; 7 AA.
 XX
 AC AAR65792;
 DE 26-JUN-1995 (first entry)
 XX Fibrin-specific epitopic peptide.
 XX KW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
 KW anti-fibrin-specific monoclonal antibodies.
 XX Synthetic.
 XX PN US5357042-A.
 XX PD 18-OCT-1994.
 XX PP 23-APR-1984; 84US-0603155.
 XX PR 23-APR-1984; 84US-0603155.
 PR 30-JAN-1986; 86US-0824228.
 PR 22-DEC-1986; 89US-0454954.
 PR 24-AUG-1994; 92US-0932729.
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX PI Haber E, Hui K, Matsueda GR;
 XX DR WPI: 1994-332411/41.
 XX PT Synthetic epitopic peptide(s) of variable length - capable of eliciting fibrin specific antibodies free of fibrinogen cross-reactivity.
 XX PT
 XX PS Claim 2; Column 18; 12pp; English.
 XX AR65789-R65794 are synthetic peptides comprising fibrin-specific epitopic sequences, they can be used to prepare hybridoma cell lines, which produce antifibrin-specific monoclonal antibodies substantially devoid of fibrinogen cross-reactivity. These antibodies are useful in the in vivo and in vitro detection of thrombi and fibrin deposits.
 XX SQ Sequence 7 AA;

Query Match 82.0%; Score 41; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR WPI; 1992-383677/47.
 XX Bi-specific antibody useful for treating thrombotic obstructive
 PT diseases e.g. cardiac infarction - Comprises antithrombin
 PT antibody variable region and anti-thrombolytic substance antibody
 PT variable region with no heavy chain constant region domains 2 and
 PT 3
 XX Disclosure: Page 3; 30pp; English.

PS This sequence represents an N-terminal peptide of human fibrin. It
 CC was used in the production of bispecific monoclonal antibodies which
 CC are specific for fibrins, but do not bind fibrinogen, and are
 CC specific for anti-thrombolytic substance. The compsn. contng. these
 CC Abs lacks the side effects of prior art Ab targetted thrombolytic
 CC agents and has enhanced thrombolytic activity.

XX Sequence 12 AA;

SQ Query Match 82.0%; Score 41; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 12
 ID AAR44829 standard; peptide; 12 AA.
 XX AAR44829
 AC AAR44829;
 XX DT 20-JUN-1994 (first entry)
 DE Human fibrin beta-chain N-terminal Peptide (1-11)-Cys.
 XX KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 OS Synthetic.

RESULT 12
 ID AAR44829 standard; peptide; 12 AA.
 XX AAR44829
 AC AAR44829;
 XX DT 20-JUN-1994 (first entry)
 DE Human fibrin beta-chain N-terminal Peptide (1-11)-Cys.
 XX KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Region 1-11
 FT /note- "human fibrin beta-chain residues 1-11"
 FT Modified-site 12
 FT /note- "BSA carrier is attached to Cys"
 PN JP05304992-A.
 PD 19-NOV-1993.
 PR 17-JUN-1992; 92JP-0158301.
 PR 20-JUN-1991; 91JP-0148936.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX WPI; 1993-408334/51.

XX Disclosure: Page 9; 38pp; Japanese.

PS Human fibrin beta-chain N-terminal Peptide (1-11)-Cys was
 CC synthesised and coupled to BSA for injection into mice. The peptide
 CC was used to raise antibodies to human fibrin. Monoclonal antibodies
 CC specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins

CC lacking the finger, EGF and Kringle 1 domains.
 XX Sequence 12 AA;
 Query Match 82.0%; Score 41; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 13
 ID AAR44838
 DE Human fibrin beta-chain peptide B.
 XX DT 20-JUN-1994 (first entry)
 DE Human fibrin beta-chain peptide B.
 XX KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 OS Synthetic.

XX JP05304992-A.
 PN JP05304992-A.
 XX PD 19-NOV-1993.
 XX PP 17-JUN-1992; 92JP-0158301.
 XX PR 20-JUN-1991; 91JP-0148936.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX DR WPI; 1993-408334/51.
 XX Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX Sequence 12 AA;
 PS Example 1; Page 14; 38pp; Japanese.
 CC Human fibrin beta-chain peptides A and B were synthesised and coupled
 CC to BSA for injection into mice. The peptides were used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
 CC are used in the production of bispecific monoclonal antibodies
 CC which also recognise truncated tPA muteins lacking the finger, EGF and
 CC Kringle 1 domains.
 XX SQ Sequence 12 AA;
 PS Query Match 82.0%; Score 41; DB 14; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 0.078;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 6 GHRPLDK 12

RESULT 14
 ID AAR44830
 DE AAR44830 standard; peptide; 16 AA.
 XX AC AAR44830;
 XX DT 20-JUN-1994 (first entry)

DE Human fibrin beta-chain internal peptide fragment.
 XX Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolytic
 KW anti-thrombotic agent; bispecific antibody.
 OS Synthetic.
 XX JP05304992-A.
 PN PD 19-NOV-1993.
 XX 17-JUN-1992; 92JJP-015301.
 PR 20-JUN-1991; 91JJP-0148936.
 XX PT (TAKE) TAKEDA CHEM IND LTD.
 PA DR WPI; 1993-408334/51.
 XX PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen.
 XX Disclosure; Page 9; 38pp; Japanese.
 XX Human fibrin internal peptide fragment was identified as a
 CC candidate immunogen to raise antibodies to human fibrin. Monoclonal
 CC antibodies specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins
 CC lacking the finger, EGF and Kringle 1 domains.
 XX Sequence 16 AA:
 SQ Query Match 82.0%; Score 41; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 1 GHRPLDK 7
 DR 1 GHRPLDK 7

Search completed: June 16, 2003, 16:03:14
 Job time : 32 secs

RESULT 15
 AAR40010
 ID AAR40010 standard; Peptide; 28 AA
 XX AAR40010;
 AC XX
 DT 23-MAY-1994 (first entry)
 XX Scintigraph imaging agent specific binding Peptide.
 DE XX
 KW Reagent; site imaging; technetium-99M labelled; peptide.
 XX Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 28 /note= "C-terminal amide"
 XX WO9121962-A.
 PN XX
 PD 11-NOV-1993.
 XX PF 19-APR-1993; 93WO-US01687.
 XX PR 30-APR-1992; 92US-0871282.
 XX PA (DIAT-) DIATECH INC.
 XX Buttram S, Civitello ER, Dean RT, Lister-James J, McBride W,
 PI XX

Gencore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2003, 16:02:14 ; Search time 11.7333 Seconds
(without alignments)
20.061 Million cell updates/sec

Title: US-09-424-940A-2
Perfect score: 50
Sequence: 1 GHRPLDKC 8

Scoring table: BLUSUM62
Gapop 10.0 , Gapext 0.5

Searched: 265574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database : Issued_Patents_AAs:
1: /cgns_6/piodata/1/1aa/5A_COMB.pep:
2: /cgns_6/piodata/1/1aa/5B_COMB.pep:
3: /cgns_6/piodata/1/1aa/6A_COMB.pep:
4: /cgns_6/piodata/1/1aa/6B_COMB.pep:
5: /cgns_6/piodata/1/1aa/pctrus.COMB.pep:
6: /cgns_6/piodata/1/1aa/backfiles1.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	50	100.0	8	1 US-09-058-699-11	Sequence 11, Appli
2	41	82.0	7	1 US-08-058-599-10	Sequence 10, Appli
3	41	82.0	10	2 US-08-448-547-1	Sequence 11, Appli
4	41	82.0	28	1 US-08-486-135-12	Sequence 12, Appli
5	41	82.0	28	1 US-08-470-152-12	Sequence 12, Appli
6	41	82.0	28	1 US-08-468-36B-10	Sequence 10, Appli
7	41	82.0	28	2 US-07-871-282A-10	Sequence 10, Appli
8	41	82.0	28	2 US-08-290-853-33	Sequence 33, Appli
9	41	82.0	28	2 US-08-253-678A-10	Sequence 10, Appli
10	41	82.0	28	3 US-08-582-134B-10	Sequence 10, Appli
11	41	82.0	28	3 US-08-170-239-10	Sequence 10, Appli
12	41	82.0	30	2 US-08-290-953-35	Sequence 35, Appli
13	41	82.0	31	1 US-08-472-535-9	Sequence 9, Appli
14	41	82.0	31	1 US-08-484-774-9	Sequence 9, Appli
15	41	82.0	31	3 US-08-266-178A-9	Sequence 9, Appli
16	41	82.0	491	1 US-08-206-176-4	Sequence 4, Appli
17	34	68.0	9	4 US-09-258-154-234	Sequence 234, Appli
18	34	68.0	9	4 US-09-042-107-234	Sequence 234, Appli
19	34	68.0	245	4 US-08-469-360A-38	Sequence 38, Appli
20	34	68.0	378	2 US-09-055-097-1	Sequence 1, Appli
21	33	66.0	353	2 US-08-758-821-6	Sequence 6, Appli
22	33	66.0	353	4 US-09-107-858-6	Sequence 4, Appli
23	32	64.0	20	1 US-08-644-556-4	Sequence 2, Appli
24	32	64.0	2183	1 US-08-348-891A-7	Sequence 7, Appli
25	32	64.0	2183	2 US-08-905-817-7	Sequence 7, Appli
26	32	64.0	2763	3 US-08-496-444-2	Sequence 2, Appli
27	31	62.0	66	4 US-09-177-249-296	Sequence 296, Appli

ALIGNMENTS

RESULT 1
US-08-058-699-11
Sequence 11, Application US/08058699
; Patent No. 5413827

GENERAL INFORMATION:

APPLICANT: Edgar Haber
APPLICANT: Christoph Bode

TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
TITLE OF INVENTION: THROMBIN

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/058, 699
FILING DATE: 19930503
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser, Ph.D.
REGISTRATION NUMBER: 34,819
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE/DOCET NUMBER: 05433/004001
LENGTH: 8
TYPE: AMINO ACID
STRANDEDNESS:
TOPLOGY: Linear
US-08-058-699-11

Query Match Best Local Similarity Score 50%; DB 1; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Sequence 85, App

RESULT 2

Qy 1 GHRPLDKC 8
 |||||||
 Db 1 GHRPLDKC 8

US-08-058-699-10
 ; Sequence 10, Application US/08058699
 ; Patent No. 5443827

GENERAL INFORMATION:
 APPLICANT: Edgar Haber
 APPLICANT: Christoph Bode
 APPLICANT: Marshall S. Runge
 TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF THROMBIN

NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2104

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (version 5.1)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/058,699
 FILING DATE: 19930503
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: N/A
 FILING DATE: N/A

ATTORNEY/AGENT INFORMATION:
 NAME: Janis K. Fraser, Ph.D.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 05433/004001

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: (617) 542-8906
 TELEFAX: 200154
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: Linear

US-08-058-699-10

Query Match 82.0%; Score 41; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 |||||||
 Db 1 GHRPLDK 7

RESULT 3

US-08-448-547-1
 ; Sequence 1, Application US/08448547
 ; Patent No. 5831068

GENERAL INFORMATION:
 APPLICANT: Soe, Gilbu
 APPLICANT: Kohno, Isao
 APPLICANT: Inuzuka, Kimiko
 APPLICANT: Ito, Yumiko
 TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
 TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:

US-08-448-547-1
 ; Sequence 1, Application US/08448547
 ; Patent No. 5831068

GENERAL INFORMATION:
 APPLICANT: Soe, Gilbu
 APPLICANT: Kohno, Isao
 APPLICANT: Inuzuka, Kimiko
 APPLICANT: Ito, Yumiko
 TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
 TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:

RESULT 4

US-08-448-547-1
 ; Sequence 12, Application US/084486135
 ; Patent No. 572034

GENERAL INFORMATION:
 APPLICANT: Dean, Richard T
 APPLICANT: Buttram, Scott
 APPLICANT: McBride, William
 APPLICANT: Lister-Jones, John
 APPLICANT: Civitello, Edgar R
 APPLICANT: Banner & Allegretti, Ltd.

TITLE OF INVENTION: Technetium-99m Labeled Peptides for Imaging
 NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,135

FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 572093nhan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,205-N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEX: 910-221-5317
 FAX: 312-715-1234
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-486-135-12

Query Match Score 82.0%; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 5
 US-08-470-152-12
 ; Sequence 12, Application US/08470152
 ; Patent No. 5780007
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 APPLICANT: Buttram, Scott
 APPLICANT: McBride, William
 APPLICANT: Lister-James, John
 APPLICANT: Civitello, Edgar R.
 TITLE OF INVENTION: Technetium-99m Labeled Peptides for Imaging
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Allegretti, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,152
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5780007nhan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,205-L
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEX: 910-221-5317
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-470-152-12

Query Match Score 82.0%; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 6
 US-08-468-964B-10
 ; Sequence 10, Application US/08468964B
 ; Patent No. 5722303
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 APPLICANT: Buttram, Scott
 APPLICANT: McBride, William
 APPLICANT: Lister-James, John
 APPLICANT: Civitello, Edgar R.
 TITLE OF INVENTION: Technetium-99m Labeled Peptides for Imaging
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Diatide, Inc.
 STREET: 9 Delta Drive
 CITY: Londonderry
 STATE: NH
 COUNTRY: USA
 ZIP: 03053

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,964B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniel, Patricia A.
 REGISTRATION NUMBER: 33,194
 REFERENCE/DOCKET NUMBER: DTRI 111D4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (603) 437-8970
 TELEFAX: (603) 437-8971
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-468-964B-10

Query Match Score 82.0%; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 7
 US-07-871-282A-10
 ; Sequence 10, Application US/07871282A
 ; Patent No. 5965107
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 APPLICANT: Buttram, Scott
 APPLICANT: McBride, William
 APPLICANT: Lister-James, John
 APPLICANT: Civitello, Edgar R.
 TITLE OF INVENTION: Technetium-99m Labeled Peptides for Imaging
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Diatide, Inc.
 STREET: 9 Delta Drive
 CITY: Londonderry
 STATE: NH
 COUNTRY: USA
 ZIP: 03053

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,152
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5780007nhan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,205-L
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEX: 910-221-5317
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-470-152-12

Query Match Score 82.0%; Length 28;

TITLE OF INVENTION: Imaging
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Diatide, Inc.
 STREET: 9 Delta Drive
 CITY: Londonderry
 STATE: NH
 COUNTRY: USA
 ZIP: 03053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/871,282A
 FILING DATE: 20-APR-1992
 CLASSIFICATION: A24
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniels, Patricia A.
 REGISTRATION NUMBER: 33,194
 REFERENCE/DOCKET NUMBER: DITI 111
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (603) 437-8970
 TELEFAX: (603) 437-8977
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 55-07-671-282A-10

Query Match	Match	Score	DB 2;	Length
Best Local Similarity	82.0%	41;	0.15;	
Matches	100.0%	Pred. No.	Mismatches	0;
7;	0;			
Conservative	0;			

1 GHRPLDK 7
 |||||
 1 GHRPLDK 7

RESULT 8
 1-08-290-853-33
 Sequence 33, Application US/08290853
 Patent No: 598519
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T
 APPLICANT: Buttram, Scott
 TITLE OF INVENTION: Technetium-99m Labeled Peptides
 TITLE OF INVENTION: Imaging Inflammation
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Allegretti, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/290,853
 FILING DATE: 11-OCT-1994
 CLASSIFICATION: A24
 ATTORNEY/AGENT INFORMATION:
 NAME: 598519nsh, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92 112-H

```

TELECOMMUNICATION INFORMATION:
    TELEPHONE: 312-715-1000
    TELEFAX: 312-715-1234
    TELEX: 910-221-317
    INFORMATION FOR SEQ ID NO: 33:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 28 amino acids
            TYPE: amino acid
            TOPOLOGY: linear
        MOLECULE TYPE: peptide
        FEATURE:
            NAME/KEY: Modified-site
            LOCATION: 1
            OTHER INFORMATION: /label="OTHER INFORMATION"
            /note="OTHER INFORMATION: radiolab"
        FEATURE:
            NAME/KEY: Modified-site
            LOCATION: 28
            OTHER INFORMATION: /label="OTHER INFORMATION"
            /note="OTHER INFORMATION: amide"
        US-08-290-853-33

Query Match          82.0%   S
Best Local Similarity 100.0%  S
Matches      7; Conservative 0;
Qy           1 GHRPLDK 7
Db           1 GHRPLDK 7

RESULT 9
US-08-253-678A-10
    Sequence 10, Application US/08253
    Patent No. 5597844
    GENERAL INFORMATION:
        DEAN, Richard T.
        APPLICANT: Buttram, Scott
        APPLICANT: McBride, William
        APPLICANT: Lister-James, John
        APPLICANT: Civitello, Edgar R.
        TITLE OF INVENTION: TECHNETIUM
        TITLE OF INVENTION: IMAGING
        NUMBER OF SEQUENCES: 23
        CORRESPONDENCE ADDRESS:
            ADDRESS: Diatide, Inc.
            STREET: 9 Delta Drive
            CITY: Londonderry
            STATE: NH
            COUNTRY: USA
            ZIP: 03053
        COMPUTER READABLE FORM:
            MEDIUM TYPE: FLOPPY disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: Patentin Release
            CURRENT APPLICATION DATA:
                APPLICATION NUMBER: US/08/2
                FILING DATE: 03-JUN-1994
                CLASSIFICATION: 424
                ATTORNEY/AGENT INFORMATION:
                    NAME: McDaniels, Patricia A.
                    REGISTRATION NUMBER: 33-194
                    REFERENCE/DOCKET NUMBER: DT
                TELECOMMUNICATION INFORMATION:
                    TELEPHONE: (603) 437-8970
                    TELEFAX: (603) 437-8977
                INFORMATION FOR SEQ ID NO: 10:
                    SEQUENCE CHARACTERISTICS:
                        LENGTH: 28 amino acids
                        TYPE: amino acids

```

STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-253-678A-10

Query Match Score 41; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 10
 US-08-582-134B-10
 Sequence 10, Application US/08582134B
 Patent No. 6074627
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T.
 APPLICANT: Buttram, Scott
 APPLICANT: McBride, William
 APPLICANT: Lister-James, John
 APPLICANT: Civitello, Edgar R.
 TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Diatide, Inc.
 STREET: 9 Delta Drive
 CITY: Londonderry
 STATE: NH
 COUNTRY: USA
 ZIP: 03053

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/582,134B
 FILING DATE: 14-MAY-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniels, Patricia A.
 REGISTRATION NUMBER: 33,194
 REFERENCE/DOCKET NUMBER: DTII 112D1
 TELEPHONE: (603) 437-8970
 TELEFAX: (603) 437-8977
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-582-134B-10
 Query Match Score 41; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 11
 US-08-170-299-10
 Sequence 10, Application US/08170299
 Patent No. 6086849
 GENERAL INFORMATION:

APPLICANT: Dean, Richard T.
 APPLICANT: Buttram, Scott
 APPLICANT: McBride, William
 APPLICANT: Lister-James, John
 APPLICANT: Civitello, Edgar R.
 TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Allegretti & Witcoff, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/170,299
 FILING DATE: 09-FEB-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6086849nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92, 205-H
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 TELEX: 910-221-5317
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-170-299-10
 Query Match Score 41; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 12
 US-08-290-853-35
 Sequence 35, Application US/08290853
 Patent No. 5989319
 GENERAL INFORMATION:
 APPLICANT: Buttram, Scott
 APPLICANT: Dean, Richard T.
 TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Allegretti, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: Illinois
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/290,853

FILING DATE: 11-OCT-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 598519an, Kevin E.
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,112-H
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEX: 910-221-5317
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 amino acids
 OTHER INFORMATION: /label= Picolinoyl
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE: Modified-site
 LOCATION: 1..3
 NAME/KEY: Modified-site
 LOCATION: 1..3
 OTHER INFORMATION: /label= Picolinoyl
 LENGTH: 30 amino acids
 OTHER INFORMATION: /note= "The amino terminal residue is
 protected by an acetamidomethyl group."
 OTHER INFORMATION: protected by an acetamidomethyl group.
 FEATURE: Modified-site
 LOCATION: 30
 OTHER INFORMATION: /label= Amide
 OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
 amide."
 OTHER INFORMATION: amide
 US-08-290-853-35

Query Match Score 41; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 11111
 3 GHRPLDK 9

RESULT 13
 US-08-472-535-9
 Sequence 9, Application US/08472535
 ; Patent No. 571191
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Richard T.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Buttram, Scott S.
 ; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 ; TITLE OF INVENTION: Imaging Inflammation
 ; NUMBER OF SEQUENCES: 17
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,774
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NO. 5807538an, Kevin E.
 ; REGISTRATION NUMBER: 35,303
 ; TELEPHONE: 312-715-1000
 ; TELEFAX: 312-715-1234
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE: Modified-site
 ; LOCATION: 1..3
 ; NAME/KEY: Modified-site
 ; OTHER INFORMATION: /label= Picolinoyl
 ; OTHER INFORMATION: /note= "The amino terminal residue is
 ; protected by an acetamidomethyl group."
 ; OTHER INFORMATION: protected by an acetamidomethyl group.
 ; OTHER INFORMATION: /label= Picolinoyl
 ; OTHER INFORMATION: /note= "The amino terminal residue is
 ; protected by an acetamidomethyl group."
 ; OTHER INFORMATION: protected by an acetamidomethyl group.

Query Match Score 41; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 11111
 4 GHRPLDK 10

RESULT 14
 US-08-472-774-9
 Sequence 9, Application US/08484774
 ; Patent No. 5807538
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Richard T.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Buttram, Scott S.
 ; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 ; TITLE OF INVENTION: Imaging Inflammation
 ; NUMBER OF SEQUENCES: 17
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,774
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NO. 5807538an, Kevin E.
 ; REGISTRATION NUMBER: 35,303
 ; TELEPHONE: 312-715-1000
 ; TELEFAX: 312-715-1234
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE: Modified-site
 ; LOCATION: 1..3
 ; NAME/KEY: Modified-site
 ; OTHER INFORMATION: /label= Picolinoyl
 ; OTHER INFORMATION: /note= "The amino terminal residue is
 ; protected by an acetamidomethyl group."
 ; OTHER INFORMATION: protected by an acetamidomethyl group.
 ; OTHER INFORMATION: /label= Picolinoyl
 ; OTHER INFORMATION: /note= "The amino terminal residue is
 ; protected by an acetamidomethyl group."
 ; OTHER INFORMATION: protected by an acetamidomethyl group.

; OTHER INFORMATION: residue is protected by an acetamidomethyl

; US-08-484-774-9

; Query Match 82.0%; Score 41; DB 1; Length 31;

; Best Local Similarity 100.0%; Pred. No. 0.17;

; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7

Db 4 GHRPLDK 10

; RESULT 15

; US-08-266-178A-9

; Sequence 9, Application US/08266178A

; Patent No. 6017510

; GENERAL INFORMATION:

; APPLICANT: Dean, Richard T

; TITLE OF INVENTION: Technetium-99m Labeled Peptides for

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Allegretti, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/266,178A

; FILING DATE: 27-JUN-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6017510; Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 92,112

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 910-221-3317

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 31 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE: Modified-site

; NAME/KEY: 1..3

; OTHER INFORMATION: /label= Picolinoyl

; OTHER INFORMATION: /note= "The amino terminal residue is

; OTHER INFORMATION: Pyridine-2-carbonyl; the thiol of the cysteine

; OTHER INFORMATION: residue is protected by an acetamidomethyl

; US-08-266-178A-9

; Query Match 82.0%; Score 41; DB 3; Length 31;

; Best Local Similarity 100.0%; Pred. No. 0.17;

; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7

Db 4 GHRPLDK 10

Scoring table:	BLOSUM62				
Gapopen:	10.0				
Gapext:	0.5				
Searched:	283224 seqs, 96134422 residues				
Total number of hits satisfying chosen parameters:	283224				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries				
Database :	PIR_73: 1: Pirl: 2: Pir2: 3: Pir3: 4: Pir4: *				
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	41	82.0	31	2 A03297	fibrinogen beta ch
2	41	82.0	491	1 FGABD	fibrinogen beta ch protein F18014.27
3	39	78.0	725	2 A86328	hypothetical prote
4	37	74.0	892	2 D82773	probable cytochrom
5	37	74.0	482	2 T15129	hypothetical prote
6	37	74.0	518	2 BB4514	hypothetical prote
7	37	74.0	591	2 S73790	probable transcrip
8	36	72.0	201	2 C95399	hypothetical prote
9	36	72.0	240	2 AE632	fibrinogen beta ch
10	36	72.0	468	1 FGBOB	multi resistance p
11	36	72.0	1490	2 T47840	fibrinogen beta ch
12	35	70.0	463	2 A38463	hypothetical prote
13	35	70.0	562	2 T21807	probable inegrase
14	35	70.0	615	2 D96499	probable inegrase
15	35	70.0	1071	2 T18307	hypothetical prote
16	34	68.0	122	1 WILAI	zinc finger protei
17	34	68.0	130	1 TNLJGG	phospholipase A2 (
18	34	68.0	130	2 S12157	hypothetical prote
19	34	68.0	409	2 F9085	trans-activating t
20	34	68.0	416	2 AB5684	probable inegrase
21	34	68.0	421	2 T29789	hypothetical prote
22	34	68.0	673	2 T40817	zinc finger protei
23	34	68.0	782	2 JC7284	phospholipase A2 (
24	34	68.0	795	2 AB4608	hypothetical prote
25	34	68.0	911	2 T29134	hypothetical prote
26	34	68.0	1576	2 T03277	pol protein - yes
27	33	66.0	225	2 A75550	Mutt/nudix family
28	33	66.0	325	2 H95278	conserved hypothet
29	33	66.0	326	2 C98346	hypothetical prote

A; Reference number: A43568; MUID:91344740; PMID:2102623
A; Accession: B4568
A; Molecule type: DNA
A; Residues: 9-191, 'P', 193-491 <CHU>
A; Cross-references: GB:J00129; NID:9182429; PIDN:AAA52429_1; PID:g162430
R Huber, P.; DaImon, J.; Courtots, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A; Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu
A; Reference number: A90469; MUID:83283433; PMID:688356
A; Accession: A90469
A; Molecule type: DNA
A; Residues: 1-38 <CH1>
A; Accession: B90469
A; Molecule type: mRNA
A; Residues: 9-191, 'A', 193-491 <CH2>
A; Cross-references: GB:J00129; NID:9182429; PIDN:AAA52429_1; PID:g162430
R; Henschien, A.; Lottspeich, F.; Southan, C.; Tøffer-Petersen, E., ed., pp.51-56, Pe
Nucleic Acids Res. 15, 1615-1625, 1987
A; Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A; Reference number: I37389; MUID:87146483; PMID:3029722
A; Accession: I37389
A; Status: translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-38 <HDS>
A; Cross-references: EMBL:X05018; NID:931400; PIDN:CAA28674_1; PID:g31401
R; Henschien, A.; Lottspeich, F.; Southan, C.; Tøffer-Petersen, E., ed., pp.51-56, Pe
Biochemistry 16, 68-76, 1979
A; Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
A; Reference number: A94433
A; Contents: carbohydrate binding
A; Accession: A94433
A; Molecule type: protein
A; Residues: 31-137, 'QS', 140-144, 'QF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
R; Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A; Title: Disulfide bridges in the NH-2-terminal part of human fibrinogen.
A; Reference number: A90437; MUID:79124640; PMID:420779
A; Accession: A90437
A; Molecule type: protein
A; Residues: 31-112, 'E', 114-137, 'QS', 140-144, 'QF', 147-148 <BLO>
R; Henschien, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A; Title: Covalent structure of fibrinogen.
A; Reference number: A90037; MUID:83244370; PMID:6575689
A; Contents: annotation; review; disulfide bonds
R; Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
Bur. J. Biochem. 77, 595-610, 1977
A; Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
A; Reference number: A91249; MUID:77245999; PMID:891553
A; Contents: annotation; disulfide bonds
R; Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
in regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Foit
A; Title: The structures of fibrinogen and fibrin.
A; Reference number: A94437
A; Contents: annotation; disulfide bonds
R; Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984

A; Reference number: A86328

A; Accession: A86328

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-482 <BEN>

A; Cross-references: GB:AE005172; NID:98778424; PIDN:AAF79432.1; GSPDB:GN00141

A; Genetics:

A; Gene: F18014.27

A; Map position: 1

Query Match Score 39; DB 2; Length 725;

Best Local Similarity 75.0%; Pred No. 11; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8

Db 555 GHKEPDKC 562

RESULT 4

D82773

hypothetical protein Xf0702 [Imported] - *Xylella fastidiosa* (strain 9a5c)C; Species: *Xylella fastidiosa*

C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C; Accession: D82773

R; Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen-

Nature 406, 151-157, 2000

A; Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A; Reference number: A82515; MUID:20365717; PMID:10910347

A; Note: for a complete list of authors see reference number A59328 below

A; Accession: D82773

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-82 <SIM>

A; Cross-references: GB:AE003913; GB:AEE003849; NID:99105578; PIDN:AAF83512.1; GSPDB:GN001

A; Experimental source: strain 9a5c

A; GenBank ID: A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; R.

R; Simpson, M.R.S.; Bueno, M.R.P.; Camarao, A.A.; Carraro, D.M.; Carter, P.

A; Briones, M.R.S.; Bueno, M.R.P.; Camarao, L.E.A.; Carraro, D.M.; Carter, P.

A; Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laiga

J.A.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Marinho, C.L.; Marques, M.V.; Martins,

E.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Mendes, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

A; Authors: Oliveira, M.A.; Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

A; Authors: Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasaki

A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; da Silva, F.R.; da Silva Jr., W.A.; da Silveir

A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva Jr., W.A.; da Silveir

A; Authors: Tsuchako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.

A; Reference number: A59328

A; Contents: annotation

C; Generics:

A; Gene: XF0702

Query Match Score 37; DB 2; Length 82;

Best Local Similarity 75.0%; Pred No. 3.3; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8

Db 59 GHSPGK 66

RESULT 5

M15829

hypothetical protein C53C9.3 - *Caenorhabditis elegans*C; Species: *Caenorhabditis elegans*

C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000

C; Accession: R15829

R; Bentley, D.

A; Submitted to: the EMBL Data Library, June 1995

A; Reference number: Z18413 of *C. elegans* cosmid C53C9.

A; Accession: T15829

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-482 <BEN>

A; Cross-references: EMBL:U28734; NID:9861255; PID:91945480; PIDN:AB52604.1; GSPDB:

A; Genetics:

A; Gene: C53C9.3

A; Map position: X

A; Introns: 19/2; 49/3; 128/3; 189/2; 203/3; 254/3; 273/1; 311/2; 372/2; 449/1

A; Interv: 1

Query Match Score 37; DB 2; Length 482;

Best Local Similarity 85.7%; Pred. No. 19; Mismatches 0; Indels 1; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HRPLDKC 8

Db 155 HRPLDYC 161

RESULT 6

B84514

probable cytochrome P450 [imported] - *Arabidopsis thaliana*C; Species: *Arabidopsis thaliana* (mouse-ear cress)

C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 23-Mar-2001

C; Accession: B84514

R; Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallo

euss, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent

Nature 402, 761-768, 1999

A; Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A; Reference number: A84420; MUID:20083487; PMID:10617197

A; Accession: B84514

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-518 <STO>

A; Cross-references: GB:AE002093; NID:94587680; PIDN:ADD25850.1; GSPDB:GN00139

A; Genetics:

A; Gene: At2g14100

A; Map Position: 2

C; Superfamily: human cytochrome P450 CYPD6; cytochrome P450 homology

C; Keywords: heme; iron; metalloprotein

F; 453/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match Best Local Similarity 74.0%; Score 37; DB 2; Length 518;

Pred. No. 20;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8

Db 112 GHSPIDEC 119

RESULT 7

S73790

hypothetical protein A19_ORF591 - *Mycoplasma pneumoniae* (strain ATCC 29342)C; Species: *Mycoplasma pneumoniae*

A; Variety: ATCC 29342

C; Accession: S73790

R; Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkle, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A; Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*

A; Reference number: S73327; MUID:8948633

A; Accession: S73790

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-591 <HIM>

A; Cross-references: EMBL:AE000046; GB:U00089; NID:91674152; PIDN:AB96112.1; PID:91

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 19

C; Genetics:

A; Genetic code: SGC3

C; Superfamily: Mycoplasma pneumoniae hypothetical protein A19_ORF591

Query Match	Score	DB 2:	Length	Pred.	No. Mismatches	Indels	Gaps	O:
Best Local Similarity	74.0%	37;	591;	No. 23;				0;
Matches	75.0%							
6; Conservative	0;							
Qy	1 GHRPLDKC 8							
Db								
	240 GENPLDKC 247							

RESULT 8

C95399 Probable transcription regulator [Imported] - Sinorhizobium meliloti (strain 1021) magap

C:Species: Sinorhizobium meliloti (strain 1021) magap

C:Accession: AE006469; PIDN:AAK65757_1; PID:914524255; GSPDB:GN00165

A:Cross-references: GB:AE006469; PIDN:AAK65757_1; PID:914524255

A:Experimental source: strain 1021, megaplasmid pSymA

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A:Reference number: A95262; PMID:21396509; MUID:434812

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-201 <XUR>

A:Cross-references: GB:AE006469; PIDN:AAK65757_1; PID:914524255; GSPDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A:Reference number: A95262; PMID:21396509; MUID:434812

A:Contents: annotation

A:Gene: SMA2008

A:Genome: Plasmid

Query Match Score 72.0%:保守性 100.0%; 预测 No. 13;

Best Local Similarity 72.0%; Length 201;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O:

Qy 1 GHRPLD 6

Db | | | | |

175 GHRPLD 180

Query Match Score 72.0%:保守性 100.0%; 预测 No. 13;

Best Local Similarity 72.0%; Length 201;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O:

Qy 1 GHRPLDKC 8

Db | | | | |

144 HRPLRK 150

RESULT 9

AE2632 hypothetical protein Atu0456 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C:Accession: AE2632; PIDN:APL41475_1; PID:917738801; GSPDB:GN00186

A:Cross-references: GB:AE008688; PIDN:APL41475_1; PID:917738801; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

A:Genes: Atu0456

A:Map position: circular chromosome

Query Match Score 72.0%:保守性 100.0%; 预测 No. 28;

Best Local Similarity 72.0%; Length 468;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0; O:

Qy 1 GHRPLDK 7

Db | | | | |

22 GRPYDK 28

RESULT 11

T47840

multi resistance protein homolog - *Arabidopsis thaliana*
 N;Alternate names: protein T209;140
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
 C;Accession: T47840
 R;Nyakatura, G.; Furtmann, B.; Dauner, D.; Starr, W.; Holland, R.; Weichselgartner, M.; submitted to the Protein Sequence Database, February 2000
 A;Reference number: 224475
 A;Accession: T47840
 A;Molecule type: DNA
 A;Residues: 1-1490 <NYA>
 A;Experimental source: cultivar Columbia; BAC clone T209
 C;Genetics:
 A;Map position: 3
 A;Introns: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3; 1369/1; 1449/1
 A;Note: 1209;140
 C;Superfamily: human multidrug resistance protein cMOAT2; AtP-binding cassette homology
 Query Match 72.0%; Score 36; DB 2; Length 1490;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GHRPLDK 6
 Db 1226 GHRPLD 1231

RESULT 12
 A3B463 fibrinogen beta chain - chicken (fragment)
 C;Species: *Gallus gallus* (chicken)
 C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
 C;Accession: A3B463
 R;Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
 Biochemistry 30, 3390-3394, 1991
 A;Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage site
 A;Reference number: A3B463; MUID:91182745; PMID:2009266
 A;Accession: A3B463
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-463 <WEI>
 A;Cross-references: GB:M58514; PID:9211779; PID:AAA48770_1; PID:9211780
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide; fibrinogen disulfide ring homology <FDR>
 F;2:2-463/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 70.0%; Score 35; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 HRPLDK 7
 Db 19 HRPLDK 24

RESULT 13
 T27807 hypothetical protein ZK265.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T27807
 R;Dobson, R.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z20422
 A;Accession: T227807
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-562 <WIL>
 A;Cross-references: EMBL:Z81143; PIDN:CA03514_1; GSPDB:GN00019; CESSP:ZK265.1
 C;Experimental source: clone 2K265
 C;Genetics:

A;Gene: CESP:ZK265.1
 A;Map Position: 1
 A;Introns: 19/2; 46/3; 93/2; 219/2; 274/3; 319/2; 362/3; 431/3; 482/1
 Query Match Similarity 70.0%; Score 35; DB 2; Length 562;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GHRPLDK 8
 Db 404 GYRPIDYC 411

RESULT 14
 D96499 probable UDP-glucose:sterol glucosyltransferase [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: D96499
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewa
 anse, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Mar; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A66141; MUID:21016719; PMID:11130712
 A;Accession: D96499
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-615 <STO>
 A;Cross-references: GB:AE005173; NID:95080759; PIDN:ADD39269_1; GSPDB:GN00141
 C;Genetics:
 A;Gene: T10512_7
 A;Map position: 1

Query Match Similarity 70.0%; Score 35; DB 2; Length 615;
 Best Local Similarity 75.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GHRPLDK 8
 Db 48 GHRLDHIC 55

RESULT 15
 Q18307 suppressor protein - yeast (*Kluyveromyces marxianus* var. *lactis*)
 C;Species: *Candida sphaerica*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C;Accession: T18307
 R;Groen, K.R.; Heyman, H.C.; Steffen, M.C.; Hawkins, L.; Martin, N.C.
 Yeast 14, 77-87, 1998
 A;Title: *Kluyveromyces lactis* SBF1 and its Saccharomyces cerevisiae homologue bypass
 A;Reference number: 213599; MUID:9483797
 A;Accession: T18307
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1071 <SRO>
 A;Cross-references: EMBL:U92898; NID:92104692; PID:92104693; PIDN: AAC39353_1
 C;Genetics:
 A;Gene: SEF1
 C;Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear clus
 F;81-121/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match Similarity 70.0%; Score 35; DB 2; Length 1071;
 Best Local Similarity 62.5%; Pred. No. 1e-02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDK 8

Fri Jun 27 12:48:59 2003

us-09-424-940a-2.rpr

Page 6

Db | | |: |
 79 GHRPVSC 86

Search completed: June 16, 2003, 16:05:02
Job time : 14.3333 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	41	BLOSUM62	GaPop 10.0 , Gapext 0.5	82.0	31	1	FIBB_CANFA
2	41	searched:	112892 seqs, 41476328 residues	82.0	491	1	FIBB_HUMAN
3	37	Total number of hits satisfying chosen parameters:	112892	74.0	591	1	YD72_MICP
4	36	Minimum DB seq length: 0		72.0	468	1	FIBB_BOVIN
5	35	Maximum DB seq length: 2000000000		70.0	463	1	FIBB_CHICK
6	35	Post-processing: Minimum Match 0%		70.0	479	1	FIBB_RAT
7	35	Maximum Match 100%		70.0	1071	1	SEFB_KLULA
8	34	Listing first 45 summaries		68.0	122	1	IAAT_ELECO
9	34	Database :	SwissProt_40.1*	68.0	130	1	TAT_HVBE
10	34	SUMMARIES		68.0	130	1	TAT_HY2D1
11	34			68.0	130	1	TAT_HY2G1
12	33			66.0	895	1	DSC3_MOUSE
13	33			66.0	1581	1	LMG3_MOUSE
14	32			64.0	94	1	TAT_SIVAI
15	32			64.0	275	1	SLBP_MOUSE
16	32			64.0	288	1	YL87_GAEL
17	32			64.0	296	1	Y608_TREPA
18	32			64.0	475	1	YM61_FEAST
19	32			64.0	560	1	EFS_MOUSE
20	32			64.0	698	1	YMCA_ECOLI
21	32			64.0	785	1	SOK2_FEAST
22	32			64.0	883	1	HMDH_XENLA
23	32			64.0	1080	1	HDA4_CHICK
24	32			64.0	1084	1	HDA4_HUMAN
25	32			64.0	1295	1	GLP1_GAEL
26	32			64.0	2183	1	RRPL_MEASA
27	32			64.0	2183	1	RRPL_MEASE
28	32			64.0	5217	1	HTS1_COCCA
29	31			62.0	119	1	RM14_TETPY
30	31			62.0	168	1	MBP_RABIT
31	31			62.0	169	1	MBP_BOVIN
32	31			62.0	170	1	MFA5_BOVIN
33	31			62.0	215	1	PCP_BACSU

ALIGNMENTS						
RESULT 1						
ID	FIBB_CANFA	STANDARD;	PRT;	31 AA.		
AC	P02677;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	01-OCT-1989 (Rel. 12, Last sequence update)					
DT	15-JUN-2002 (Rel. 41, Last annotation update)					
DE	Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).					
GN	FGB.					
OS	Canis familiaris (Dog).					
OC	Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.					
OX	NCBI_TaxID=9615;					
RN						
RP						
SEQUENCE						
MEDLINE	76081726; PubMed=1198547;					
RA	Birken S., Wilner G.D., Canfield R.E.; "Studies of the structure of canine fibrinogen.";					
RT	Thromb. Res. 7:599-610(1975).					
RL						
RN	SEQUENCE OF 1-19.					
RA	Blomback B., Blomback M., Grondahl N.J.; Studies on fibrinopeptides from mammals.;					
RT	Acta Chem. Scand. 19:1789-1791(1965).					
RL						
RN	SEQUENCE OF 1-19.					
RP	Krajewski T., Blomback B.; Location of tyrosine-O-sulphate in fibrinopeptides.;					
RX	Medline=69066367; PubMed=5727635;					
RA	Acta Chem. Scand. 19:1339-1346(1968).					
RT	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.					
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.					
CC	-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.					
CC	PIR; A03123.; A03123.					
DR	PIR; A05297.; A05297.					
DR	Interpro; IPR002181; Fibrinogen C.					
DR	Prosite; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.					
KW	Blood coagulation; Plasma; Sulfation.					
FT	Peptide	1	19			
FT	Chain	20	>31			
FT	Mod_Res	2	2			
FT	Mod_Res	3	3			
FT	Non_Ter	31	31			
SQ	Sequence	31 AA;	3/31 MW;	A043727257698156 CRC64;		
	Query Match			82.0%; Score 41; DB 1; Length 31;		
	Best Local Similarity			100.0%; Pred. No. 0.067;		
	Matches			Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 GHRPLDK 7					

Db 20 GHRPLDK 26

RESULT 2

FIBB_HUMAN STANDARD; PRT; 491 AA.

ID FIBB_HUMAN STANDARD; PRT; 491 AA.

AC P02675; (Rel. 01, Created) DT 21-JUL-1986 (Rel. 26, Last sequence update) DT 01-JUL-1993 (Rel. 41, Last annotation update)

DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].

GN FGB.

OS Homo sapiens (Human).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukarya; Fungi; Primates; Catarrhini; Hominoidea; Homo.

NCBI_TaxID=9606; OX [1]

RP SEQUENCE FROM N.A. MEDLINE=91344740; PubMed=2102623;

RA Chung D.W., Harris J.E., Davie E.W.; "Nucleotide sequences of the three genes coding for human fibrinogen." RT

RA Adv. Exp. Med. Biol. 281:39-48(1990).

RN [2]

RP SEQUENCE FROM N.A. MEDLINE=93283433; PubMed=6688356;

RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.; "Characterization of complementary deoxyribonucleic acid and genomic deoxyribonucleic acid for the beta chain of human fibrinogen." RT

RA Biochemistry 22:3244-3250(1983).

RN [3]

RP SEQUENCE FROM N.A. MEDLINE=93283433; PubMed=6688356;

RA Chung D.W., Harris J.E., Davie E.W.; "Nucleotide sequences of the three genes coding for human fibrinogen." RT

RA (In) Liu C.Y., Chien S. (eds.); "Fibrinogen, thrombosis, coagulation and fibrinolysis," pp.39-48, Plenum Press, New York (1991).

RN [4]

RP SEQUENCE FROM N.A., AND VARIANT SER-100; HIS-170; LEU-265 AND RP LYS-78. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A.; "Submission (JUN-2001) to the EMBL/GenBank/DBJ databases." RL [5]

RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE. RA Henschel A., Lottspeich F., Southan C., Topfer-Petersen E.; "Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural variants." RT

RA (In) Peeters H. (eds.); "Proteins of biological fluids," Proc. 28th colloquium, pp.51-56, Pergamon Press, Oxford (1980).

RL [6]

RP SEQUENCE OF 31-491. MEDLINE=79124640; PubMed=420779;

RA Watt K.W.K., Takagi T., Doolittle R.F.; "Amino acid sequence of the beta chain of human fibrinogen." RT

RA Biochemistry 18:68-76(1979).

RP SEQUENCE OF 31-148, AND DISULFIDE BONDS. MEDLINE=76225080; PubMed=936108;

RA Blomback B., Hessel B., Hogg D.; "Disulfide bridges in NH2-terminal part of human fibrinogen." RT

RA Thromb. Res. 8:639-658(1976).

RN [7]

RP SEQUENCE OF 1-38 FROM N.A. MEDLINE=87146483; PubMed=3029722;

RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z., Marquerie G.; "Characterization of the 5'-flanking region for the human fibrinogen gene." RT

RT Nucleic Acids Res. 15:1615-1625(1987).

RL [8]

[9] SEQUENCE OF 31-44. Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.; "Studies on fibrinopeptides from primates." Acta Chem. Scand. 19:1788-1789(1965).

RA [10]

RP REVIEW, AND DISULFIDE BONDS. RX MEDLINE=8354370; PubMed=575689;

RA Henschel A., Lottspeich F., Kehl M., Southan C.; "Covalent structure of fibrinogen." Ann. N.Y. Acad. Sci. 408:28-43(1983).

RA [11]

RP DISULFIDE BONDS. RX MEDLINE=7724599; PubMed=891553;

RA Gardlund B., Hessel B., Marguerie G., Murano G., Blomback B.; "Primary structure of human fibrinogen. Characterization of disulfide-containing cyanogen-bromide fragments." Bur. J. Biochem. 77:595-610(1977).

RA [12]

RP DISULFIDE BONDS. RX Doolittle R.F., Takagi T., Watt K.W.K., Bouma H., III, Cottrell B.A., Cassman K.G., Goldbaum D.M., Doolittle J.R., Friesz S.J.; "The structures of fibrinogen and fibrin." (In) Magnusson S., Ottesen M., Foltmann B., Dano K., Neurath H. (eds.); "Regulatory proteolytic enzymes and their inhibitors," Bergamon Press, New York (1978).

RA [13]

RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS. RX MEDLINE=84105751; PubMed=6383144;

RA Doolittle R.F.; "Fibrinogen and fibrin." Annu. Rev. Biochem. 53:195-229(1984).

RA [14]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491. RX MEDLINE=9712408; PubMed=333233;

RA Spraggan G., Everse S.J., Doolittle R.F.; "Crystal structures of fragment D from human fibrinogen and its crosslinked counterpart from fibrin." RT

RA Nature 389:455-462(1997).

RA [15]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491. RX MEDLINE=98392395; PubMed=9628725;

RA Spraggan G., Everse S.J., Veerapandian L., Riley M., Doolittle R.F.; "Conformational changes in fragments D and double-D from human fibrinogen upon binding the peptide ligand Gly-His-Pro-amide." RT

RA Biochemistry 37:8637-8642(1998).

RA [16]

RP X-RAY CRYSTALLOGRAPHY. RX MEDLINE=99175088; PubMed=10074346;

RA Everse S.J., Spraggan G., Veerapandian L., Doolittle R.F.; "Crystal structure of fragment double-D from human fibrin with two different bound ligands." RT

RA Biochemistry 38:2941-2946(1999).

RA [17]

RP VARIANT BALTIMORE-2. RX MEDLINE=8958942; PubMed=3194892;

RA Schmelzer C.H., Ebert R.F., Bell W.R.; "Beta polymorphism at B beta 448 of fibrinogen identified during structural studies of fibrinogen Baltimore II." RT

RA Asakura S., Shirakawa S.; "A new congenital abnormal fibrinogen Ise characterized by the replacement of B beta 1 glycine-15 by cysteine." RT

RA Blood 77:1958-1963(1991).

RA [18]

RP VARIANT ISE. RX MEDLINE=91208409; PubMed=2018836;

RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.; "A variant of B beta 448 of fibrinogen II." RT

RA Asakura S., Shirakawa S.; "Structural studies of fibrinogen Baltimore II." RT

RA Thromb. Res. 52:1173-1177(1988).

RA [19]

RP VARIANT NAPLES. RX MEDLINE=92340664; PubMed=1634610;

RA Roopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;

RT "Molecular basis of fibrinogen Naples associated with defective thrombin binding and thrombophilia. Homozygous substitution of B beta 68 Ala-->Thr.";
 RT RL J. Clin. Invest. 90: 238-244(1992).
 RN [20]
 RP VARIANT LIJMUIDEN AND NIJMEGEN
 RX MEDLINE=9226809; PubMed=1565641;
 RA Koopman J., Haverkate F., Grimbbergen J., Engesser L., Novakova I., Kerst A. F. J. A., Lord S. T.;
 RA "Abnormal fibrinogens IJmuiden (B beta.Arg14-->Cys) and Nijmegen (B beta.Arg44-->Cys) form disulfide-linked fibrinogen-albumin complexes";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 RN [21]
 RP VARIANT NEW YORK-1.
 RX MEDLINE=85157605; PubMed=3156856;
 RA Liu C.Y., Kochan J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional fibrinogen with a deletion of B beta(9-72) corresponding exactly to exon 2 of the gene.;"
 RT RL J. Biol. Chem. 260:4390-4396(1985).
 CC 1- FUNCTION: FIBRINOGEN HAS A DOUBBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
 CC 1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE DIVERRGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE DISTAL DOMAINS, EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL ENDS OF THE ALPHA CHAINS.
 CC 1- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
 CC "MISCELLANEOUS: CONVERSION OF FIBRINOGEN A AND B FROM ALPHA & BETA THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIA WHICH CATALYZES THE EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT MONOMERS."
 CC 1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 DR EMBL; J00129; AAA52429.1; -
 DR EMBL; J00131; AAA98115.1; JOINED.
 DR EMBL; J00132; AAA98116.1; -
 DR EMBL; J00133; -; NOT_ANNOTATED_CDS.
 DR EMBL; AF388006; AAK624.0.1; -.
 DR EMBL; X05018; CAA28674.1; -.
 DR EMBL; M64983; AAA18024.2; -.
 DR EMBL; M26877; AAA52445.1; JOINED.
 DR EMBL; M26876; AAA52445.1; JOINED.

Query Match Score: 41; DB: 1; Length: 491;
 Best Local Similarity: 100.0%; Pred. No.: 1.1; Indels: 0; Gaps: 0;
 Matches: 7; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 1 GHRPLDK 7
 Db 45 GHRPLDK 51

AC P75409;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL protein MPN372 (A19_orf591).
 GN MPN372 OR MP464.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC NCBI_TaxID=2104;
 RN [1]
 RP Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.;"
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 DR EMBL; AE000046; AAB96112.1; -
 DR InterPro; IPR033898; Borpert_toxA.
 DR Pfam; PF02917; Pertussis_Sl_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE: 591 AA; 680591 MW; B958C85C9EE29E90 CRC64;
 Query Match Score: 37; DB: 1; Length: 591;
 Best Local Similarity: 75.0%; Pred. No.: 8.6%; Mismatches: 2; Indels: 0; Gaps: 0;
 DR GHRPLDK 8
 Db 240 GENPLDK 247

RESULT 4
 FIBB_BOVIN STANDARD; PRT; 468 AA.
 ID FIBB_BOVIN
 AC AC202676;
 DT 21-JUL-1986 (Rel. 01, Created)
 CC 1- FIBRINogen beta chain precursor [Contains: Fibrinopeptide B].
 DR 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN FGB.
 OS Bos taurus (Bovine);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-4.
 RA Blomback B., Doolittle R.F.;
 RA Sjogquist J., Blomback B., Wallen P.;
 RT "The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.";
 RT Acta Chem. Scand. 17:1816-1819(1963).
 RN [2]
 RP SEQUENCE OF 5-21.
 RA Blomback B., Doolittle R.F.;
 RA Sjogquist J., Blomback B., Wallen P.;
 RT "Amino acid sequence of bovine fibrinopeptides.";
 RT Ark. Kemi 16:425-436(1960).
 RN [3]
 RP SEQUENCE OF 22-53.
 RX MEDLINE=9164394; PubMed=434801;
 RA Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
 RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;
 RT "Amino acid sequences of portions of the alpha and beta chains of

RESULT 5		BB_CHICK		BB_CHICK		BB_CHICK	
Query Match	Match	72.0%	Score	36	DB 1;	Length	468;
Best Local	Similarity	65.7%	Pred. No.	11;			
Matches	6;	Conservative	0;	Mismatches	1;	Indels	0;
						Gaps	0;
1	GHRPLDK	7					
22	GHREPYDK	28					

DR SMART; SM00066; GAL4; 1.
 DR PROSITE; PS00463; 2N2_CY6_FUNGAL_1; 1.
 DR PROSITE; PS50048; 2N2_CY6_FUNGAL_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein; Zinc;
 KW Metal-binding.
 FT DNA_BIND 86 116 ZN(2)-CYS(6)_FUNGAL-TYPE
 SEQUENCE 1071 AA; 120031 MW; 92CB05A3F703FB53 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 1071;
 Best Local Similarity 62.5%; Pred. No. 40;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 ||||:
 Db 79 GHRPvTSC 86

RESULT 8
 TAAT_ELECO
 ID TAAT_ELECO STANDARD; PRT: 122 AA.

AC P01037;
 DT 21-JUL-1996 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha amylase/trypsin inhibitor (RATI) (RATI).
 OS Eleusine coracana (Indian finger millet) (Ragi).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Magnoliopsida; Poales; Poaceae; PACC clade;
 OC Chloridoideae; Eragrostidaceae; Eleusine.
 OC NCBI_TAXID=4511;
 RN [1]
 RP TISSUE=Seed;
 RA Campos F.A.P., Richardson M.;
 RT "The complete amino acid sequence of the bifunctional alpha-
 amylose/trypsin inhibitor from seeds of ragi (Indian finger millet),
 Eleusine coracana Gaertn.".;
 RL FEBS Lett. 152:300-304 (1983).;

RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC TISSUE=Seed;
 RX MEDLINE=90362594; PubMed=9687373;
 RA Strobl S., Maskos K., Wiegand G., Huber R., Gomis-Ruth F.X.,
 RA Glockshuber R.;
 RA "Novel strategy for inhibition of alpha-amylases: yellow meal worm
 alpha amylase in complex with the Ragi bifunctional inhibitor at 2.5 Å
 resolution.";
 RT Acta Crystallogr. D 55:25-30 (1999).;
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RC TISSUE=Seed;
 RX MEDLINE=99190826; PubMed=10089391;
 RA Gourinath S., Srinivasan A., Singh T.P.;
 RT "Structure of the bifunctional inhibitor of trypsin and alpha-amylase
 from ragi seeds at 2.9-Å resolution.";
 RL Acta Crystallogr. D 55:25-30 (1999).;
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RC TISSUE=Seed;
 RX MEDLINE=20180431; PubMed=10713515;
 RA Gourinath S., Alam N., Srinivasan A., Betzel C., Singh T.P.;
 RT "Structure of the bifunctional inhibitor of trypsin and alpha-amylase
 from ragi seeds at 2.2 Å resolution.";
 RL Acta Crystallogr. D 56:287-293 (2000).;
 RN [5]
 RP STRUCTURE BY NMR.
 RC TISSUE=Seed;
 RX MEDLINE=95122319; PubMed=7599120;
 RA Strobl S., Muelnhahn P., Bernstein R., Wiltschek R., Maskos K.,
 RA Wunderlich M., Huber R., Glockshuber R., Holak T.A.;
 RT "Determination of the three-dimensional structure of the bifunctional
 alpha-amylase/trypsin inhibitor from ragi seeds by NMR
 spectroscopy.";

RL Biochemistry 34:8281-8293 (1995).
 CC -I- FUNCTION: MAY PLAY A PROTECTIVE ROLE AGAINST ENDO- AND EXOGENOUS HYDROLYtic ACTIVITIES IN THE RAGI SEEDS.
 CC -I- TISSUE SPECIFICITY: SEEDS.
 CC -I- SIMILARITY: BELONGS TO THE CEREAL TRYPsin/ALPHA-AMYLASE INHIBITOR FAMILY.
 DR PIR; A01326; WILLAI.
 DR PDB; 1BIP; 10-JUL-95.
 DR PDB; 1BMU; 02-DEC-98.
 DR PDB; 1TMQ; 08-MAR-00.
 DR InterPro; IPR003612; AAI.
 DR Pfam; PF00234; TRYPAmyl_inhbtr.
 DR PRINTS; PRO0808; AMLASBINHBT.
 DR SMART; SM0099; AAI; 1.
 DR PROSITE; PS00426; CEREAL_TRYP_AMYL_INH; 1.
 DR PROSITE; PS00426; CEREAL_TRYP_AMYL_INH; 1.
 DR Serine protease inhibitor; Alpha-amylase inhibitor; 3D-structure.
 KW DR PROSITE; PS00426; CEREAL_TRYP_AMYL_INH; 1.
 KW Serine protease inhibitor; Alpha-amylase inhibitor; 3D-structure.
 FT DISULFID 6 55
 FT DISULFID 20 44
 FT DISULFID 29 85
 FT DISULFID 45 103
 FT DISULFID 57 114
 FT VARIANT 25 26
 FT VARIANT 28 28
 FT VARIANT 70 70 P->S.
 SQ SEQUENCE 122 AA; 13138 MW; C8ED7A01CD470E17 CRC64;
 Query Match 68.0%; Score 34; DB 1; Length 122;
 Best Local Similarity 71.4%; Pred. No. 6 8;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
 TAT_HV2BE
 ID TAT_HV2BE STANDARD;
 PRT: 130 AA.
 AC P18098;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TAR protein (Transactivating regulatory protein).
 GN TAR.
 OS Human immunodeficiency virus type 2 (isolate BEN) (HIV-2).
 OC Viruses; Retroviridae; Lentiviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90281594; PubMed=2353457;
 RA Kirchhoff F., Jentsch K., Bachmann B., Stuke A., Laloux C.,
 RA Lueke W., Stahl-Henning C., Schneider J., Niesel K., Eigen M.,
 RA Hunsmann G.,
 RT "A novel proviral clone of HIV-2: biological and phylogenetic
 relationship to other primate immunodeficiency viruses.";
 RL Virology 177:305-311 (1990).
 CC -I- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -I- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: NUCLEAR; nucleolat.
 CC -I- MISCELLANEOUS: THIS ISOLATE IS FROM A GERMAN AIDS PATIENT (WITH
 CC PREDOMINANTLY NEUROLOGICAL COMPLICATIONS) WHO WAS PROBABLY
 CC INFECTED IN MALLI.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch).

CC EMBL; M30502; AAB00741.1; -.
 CC DR HIV; M30502; TATS2EN.
 CC DR InterPro; IPR001831; HIV_Tat.
 CC DR Pfam; PF00539; Tat; 1.
 CC PRNTS; PR00055; HIVATDOMAIN.
 CC transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.

SQ SEQUENCE 130 AA; 14463 MW; 5227D62952F8A625 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 130;
 Best Local Similarity 71.4%; Pred. No. 7.2;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
 TAT_HV2D1 ID TAT_HV2D1 STANDARD; PRT; 130 AA.

AC P1759; 1111: | 2 HRPLDKC 8
 DT 01-AUG-1990 (Rel. 15, Created) 44 HRPLEPC 50

DE TAT Protein (Transactivating regulatory protein).

GN TAT.
 OS Human immunodeficiency virus type 2 (isolate Ghana-1) (HIV-2).
 OC Viruses; Retroviridae; Lentiviridae; Lentivirus.

OX NCBI_TaxID=11717; [1]

RN RP SEQUENCE FROM N.A. RX MEDLINE=90122310; PubMed=2611042;

RA Hasegawa A.; Tsujimoto H.; Maki N.; Ishikawa K.I.; Miura T.; Fukasawa M.; Miki K.; Hayami M.; AIDS Res. Hum. Retroviruses 5:593-604(1989).

DE TAT Protein (Transactivating regulatory protein).

GN TAT.
 OS Human immunodeficiency virus type 2 (isolate D194) (HIV-2).
 OC Viruses; Retrovirus; Retroviridae; Lentiviridae; Lentivirus.

OX NCBI_TaxID=11713; [2]

RN RP SEQUENCE FROM N.A. RX MEDLINE=8918631; PubMed=2467304;

RA Bliesert L.; von Brzesen H.; Dietrich U.; Adamski M.; Mix D.; Andreessen R.; Immelmann A.; Henco R.; Meichner C.; RT "Nucleolar cloning of two west African human immunodeficiency virus type 2 isolates that replicate well in macrophages: a Gambian isolate, from a patient with neurologic acquired immunodeficiency syndrome, and a highly divergent Ghanaian isolate.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2383-2387(1989).

RN SEQUENCE FROM N.A. RX Kuehne H.; Kreutz R.; Ruebsamen-Waigmann H.; RT "Nucleotide sequence of HIV-2D194, an isolate from a Gambian case of neuro-AIDS, which showed excellent growth in macrophages.";
 RL Nucleic Acids Res. 18:6142-6142(1990).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

CC TRANS ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND OR ELONGATION FROM THE LTR

CC PROMOTER.

CC -!- SUBCELLULAR LOCATION: Nucleolar; nucleolar.

CC -!- MISCELLANEOUS: THIS ISOLATE IS FROM A GAMBIAN CASE OF 'NEURO-AIDS'.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>) or send an email to license@isb-sib.ch.

CC DR EMBL; X52223; CAA3649.1; -.
 DR PIR; S12157; S12157.
 DR HIV; J04542; TATS2D194.
 DR InterPro; IPR001831; HIV_Tat.
 DR Pfam; PF00539; Tat; 1.

DR PRNTS; PR00055; HIVATDOMAIN.
 DR transcription regulation; Activator; RNA-binding; Nuclear protein;

CC CC AIDS.

DR DR SEQUENCE 130 AA; 14580 MW; 95F108B537027D67 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 130;

Best Local Similarity 71.4%; Pred. No. 7.2%; Mismatches 1; Indels 0; Gaps 0;

Db 2 HRPLDKC 8
 1111: | 44 HRPLEAC 50

RESULT 12
 DSC3_MOUSE ID DSC3_MOUSE STANDARD;

AC P55830; O55122; O55110;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)				
DE Desmocollin 3 precursor.				
DE DSC3.				
GN Musculus (Mouse).				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus;				
NCBI_TAXID=10090;				
[1]				
RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.				
RX MEDLINE=98019324; PubMed=9389456;				
RP Chidley M.A.J.; Yue K.K.M.; Gould S.; Byrne C.; Garrod D.R.; Dev. Dyn. 210:315-327(1997).				
RA [2]				
RA SEQUENCE OF 709-874 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.				
RP MEDLINE=98067789; PubMed=0404003;				
RA King I.A.; Angst B.D.; Hunt D.M.; Kruger M.; Arnemann J.; Buxton R.S.; RT "Hierarchical expression of desmosomal cadherins during stratified epithelial morphogenesis in the mouse.";				
RT Differentiation 62:83-96 (1997).				
RL CC -1- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.				
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).				
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 3A (SHOWN HERE) AND 3B; ARE PRODUCED BY ALTERNATIVE SPLICING.				
CC -1- TISSUE SPECIFICITY: FIRST EXPRESSED AT E13.0 IN EPITHELIUM OF WHISKER PADS AND EXTERNAL NARES, AND IN MOST MAURE VIBRISSE FOLLICLES 12 HOURS LATER, PROMINENTLY EXPRESSED IN WHISKERS AND TACTILE FOLLICLES ABOVE THE EYE. AT E14.5, ALSO EXPRESSED IN DEVELOPING NAILS AND TEETH AND, AT LOW LEVELS, IN VENTRAL AND LATERAL SKIN. AT E15.5, HIGHLY EXPRESSED IN GENERAL BODY EPIDERMIS AND AT E16.5, DETECTED OVER ENTIRE EMBRYO. IN THE ADULT, HIGHLY EXPRESSED IN BASAL LAYERS OF STRATIFIED CELLS.				
CC -1- DOMAIN: CALCIUM MAY BE BOUND TO THE CADHERIN-LIKE REPEATS (POTENTIAL).				
CC -1- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC DR EMBL: Y11169; CAA72045_1; -.				
DR EMBL: AJ00329; CAA0996_1; -.				
DR HSSP: P15116; INGJ.				
DR MGD: MGI:1194933; Dsc3.				
DR InterPro: IPR02126; Cadherin.				
DR InterPro: IPR00233; Cadherin_C-term.				
DR Pfam: PF00028; cadherin_5.				
DR Pfam: PF01049; Cadherin_C-term; 1.				
DR SMART: SM00112; CA_5.				
DR PROSITE: PS00232; CADHERIN_1; 3.				
DR PROSITE: PS05068; CADHERIN_2; 5.				
DR KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;				
KW Cytoskeleton; Calcium-binding; Alternative splicing.				
FT SIGNAL 1 31				
FT PROPEL 32 135				
FT CHAIN 136 895				
FT DOMAIN 136 695				
FT TRANSMEM 696 716				
FT DOMAIN 717 895				
FT DOMAIN 136 243				
FT DOMAIN 244 355				
FT DOMAIN 356 472				
Query Match Score 66.0%; Length 895;				
Best Local Similarity 62.5%; Pred. No. 83; Mismatches 2; Indels 0; Gaps				
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps				
RESULT 13				
LMG3_MOUSE STANDARD; PRT: 1581 AA..				
ID LMG3_MOUSE; Q9WTF6; STANDARD;				
AC Q9WTF6; Q9WTF6;				
DT 15-JUN-2002 (Rel. 41, Created)				
DT 15-JUN-2002 (Rel. 41, Last sequence update)				
DT 15-JUN-2002 (Rel. 41, Last annotation update)				
DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).				
GN LAMC3.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; OX NCBI_TAXID=10090;				
RN [1]				
SEQUENCE FROM N.A.				
RA Albus A.M.; Burgeson B.; Champiliaud M.-F.; Koch M.; Olson P.; RT "Mouse laminin 12 gamma 3 chain";				
RA Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.				
RN [2]				
SEQUENCE OF 1-1526 FROM N.A.				
RP MEDLINE=992539969; PubMed=10318827;				
RA Ilivanaian A.; Morita T.; Tryggvason K.; "Molecular cloning and tissue-specific expression of a novel murine laminin gamma3 chain".				
RT J. Biol. Chem. 274:14107-14111(1999).				
RL -1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.				
RL -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule. Comprising one long and three short arms with globules at each end.				
RL THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12.				
CC -1- SUBCELLULAR LOCATION: Extracellular.				
CC -1- TISSUE SPECIFICITY: Strongly expressed in capillaries and arterioles of kidney as well as in interstitial Leydig cells of testis.				
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.				
CC -1- DOMAIN: DOMAIN IV IS GLOBULAR.				
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).				
CC -1- SIMILARITY: CONTAINS 11 LAMININ EGF-LIKE DOMAINS.				
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstations on the European Bioinformatics Institute. There are no restrictions on				

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>)
or send an email to license@isb-sib.ch.

CC	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch.	QY	3 RPLDKC 8 1:1:1:1
CC	DR EMBL; AFO8372; AAF0983.1; .;	Db	870 RPVDKC 875
CC	DR HSSP; P02468; 1KQO.		
CC	DR MGI; 1344394; Lamc3.		
DR	InterPro; IPR00561; EGF-like.	RESULT 14	
DR	InterPro; IPR001886; Lamnt.	TAT_SIVAI	
DR	InterPro; IPR00034; Laminin_B.	ID TAT_SIVAI	
DR	InterPro; IPR002049; Laminin_EGF.	STANDARD;	
DR	Pfam; PF00052; laminin_B; 1.	PRT;	94 AA.
DR	Pfam; PF00053; laminin_EGF; 10.		
DR	Pfam; PF00055; laminin_Nterm; 1.		
DR	PRINTS; PRO0011; EGFLAMINN.	AC Q02838;	
DR	PRODOM; PD002082; Lamnt; 1.	DT 01-JUL-1993 (Rel. 26, Created)	
DR	SMART; SM00180; EGF_Lam; 10.	DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DR	SMART; SM00281; LamB; 1.	DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DR	SMART; SM00136; Lamnt; 1.	DE TAT protein (transactivating regulatory protein)	
DR	PROSITE; PS00022; EGF_1; UNKNOWN_8.	TAT	
DR	PROSITE; PS01186; EGF_2; 2.	OS simian immunodeficiency virus (isolate AGM / clone GRI-1) (SIV-AGM).	
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 11.	OC Viruses; Retroviridae; Lentivirus.	
KW	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Signal	RN [1]	
KW	Laminin EGF-like domain; Cell adhesion; Cell adhesion; Repeat; Signal.	RP MEDLINE-91220680; PubMed-2024476;	
FT	SIGNAL 1 28	SEQUENCE FROM N.A.	
FT	CHAIN 1 29	RA Fonsgaard, A.; Hirsch, V.M.; Allan, J.S.; Johnson, P.R.;	
FT	DOMAIN 29 279	RA A highly divergent proviral DNA clone of SIV from a distict species	
FT	DOMAIN 280 335	RT RT	
FT	DOMAIN 336 391	RT RT	
FT	DOMAIN 392 438	RT RL	
FT	DOMAIN 439 488	CC -1 FUNCTION: TRANSCRIPIONAL REGULATOR THAT ACES BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND	
FT	DOMAIN 4 489 498	CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR	
FT	DOMAIN 499 698	CC PROMOTER.	
FT	DOMAIN 685 718	CC -1 SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).	
FT	DOMAIN 719 766	CC -1 SUBCELLULAR LOCATION: Nuclear; nucleolar.	
FT	DOMAIN 767 821	CC -1 MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.	
FT	DOMAIN 822 877	CC	
FT	DOMAIN 878 927	CC This SWISS-PROT entry is copyright. It is produced through a collaboration	
FT	DOMAIN 928 975	CC between the Swiss Institute of Bioinformatics and the EMBL outstation	
FT	DOMAIN 976 1024	CC the European Bioinformatics Institute. There are no restrictions on its	
FT	DOMAIN 1025 1581	CC use by non profit institutions as long as its content is in no way	
FT	DOMAIN 1029 1046	CC modified and thus this statement is not removed. Usage by and for commercial	
FT	DOMAIN 1112 1153	CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/)	
FT	DOMAIN 1208 1231	CC or send an email to license@isb-sib.ch).	
FT	DOMAIN 1438 1468	CC	
FT	CARBOHYD 1510 1575	DR M66437; AAA91926_3; ; NOT_ANNOTATED_CDS.	
FT	CARBONYD 128 128	DR InterPro; IPR00181; HIV-Tat.	
FT	CARBONYD 304 304	DR Pfam; PF00539; rat; 1.	
FT	CARBONYD 640 640	DR PRINS; PR00055; HIVTATDOMAIN.	
FT	CARBONYD 849 849	DR Transcription regulation; Activator; RNA-binding; Nuclear protein;	
FT	CARBONYD 991 991	DR AIDS.	
FT	CARBONYD 1162 1162	DR KW SEQUENCE 94 AA; 10875 MW; D23ADFDCC8B2A0D96 CRC64;	
FT	CARBONYD 1196 1196	DR Query Match Best local Similarity 64.0%; Score 32; DB 1; Length 94;	
FT	CARBONYD 1320 1320	DR Best local Similarity 71.4%; Pred. No. 13; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
FT	CARBONYD 1514 1514	DR SQ SEQUENCE 94 AA; 2 HRPLDKC 8	
FT	CONFLICT 9 9	DB 15 HRPLQPC 21	
FT	CONFLICT 190 190	RESULT 15	
FT	CONFLICT 195 195	SLBP_MOUSE	
FT	CONFLICT 221 221	ID SLBP_MOUSE	
FT	CONFLICT 394 394	STANDARD;	
FT	CONFLICT 471 471	PRT;	275 AA.
FT	CONFLICT 1150 1150	AC P97440;	
FT	CONFLICT 1387 1387	DT 16-OCT-2001 (Rel. 40, Created)	
FT	CONFLICT 1438 1438	DT 16-OCT-2001 (Rel. 40, Last sequence update)	
FT	CONFLICT 1479 1479	DT 16-OCT-2001 (Rel. 40, Last annotation update)	
FT	SEQUENCE 1581 AA; 172316 MW; 51DFADLF95EAE81 CRC64;	DE Histone RNA hairpin-binding protein (Histone stem-loop binding protein).	
FT	SEQUENCE 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	DE DE protein.	
FT	SEQUENCE 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	GN HBP OR SLBP.	
FT	SEQUENCE 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	OS Mus musculus (Mouse).	
FT	SEQUENCE 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
FT	SEQUENCE 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.	
FT	SEQUENCE 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	NCBI_TAXID=10090;	

Query Match 66.0%; Score 33; DB 1; Length 1581;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RN
 SEQUENCE FROM N.A. TISSUE=Embryo;
 RP
 STRAIN=N.I.H. Swiss; TISSUE=Embryo;
 RC
 MEDLINE=9711584; PubMed=8957003;
 RX
 Wang Z.-F., Whitfield M.L., Ingledue T.C. III, Dominski Z.,
 RA
 Marzluff W.F.;
 RA
 "The protein that binds the 3' end of histone mRNA: a novel
 RNA-binding protein required for histone pre-mRNA processing.";
 RT
 RNA-binding protein required for histone pre-mRNA processing.
 RL
 Genes Dev. 10:3028-3040 (1996).
 CC
 FUNCTION: BINDS THE STEM-LOOP STRUCTURE OF REPLICATION-DEPENDENT
 HISTONE PRE-MRNAs AND CONTRIBUTES TO EFFICIENT 3' END PROCESSING
 BY STABILIZING THE COMPLEX BETWEEN HISTONE PRE-MRNA AND U7 SMALL
 NUCLEAR RIBONUCLEOPROTEIN (SNRNP). COULD PLAY AN IMPORTANT ROLE IN
 TARGETING MATURE HISTONE mRNA FROM THE NUCLEUS TO THE CYTOPLASM
 AND TO THE TRANSLATION MACHINERY. STABILIZES MATURE HISTONE mRNA
 AND COULD BE INVOLVED IN CELL-CYCLE REGULATION OF HISTONE GENE
 EXPRESSION (BY SIMILARITY).
 CC
 -I- SUBUNIT: MONOMER.
 CC
 -I- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC (POLYRIBOSOME-
 ASSOCIATED).
 CC
 -I- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC
 -I- SIMILARITY: BELONGS TO THE SLBP FAMILY.
 CC
 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 DR
 EMBL; U75680; AAC53530.1; -
 DR
 MGD; MGI:108402; Slbp.
 KW
 RNA-binding; mRNA processing; Nuclear protein; Phosphorylation.
 FT
 MOD_RES 62 62 PHOSPHORYLATION (BY CDCC2) (BY
 SIMILARITY).
 FT
 DOMAIN 129 198 RNA-BINDING (BY SIMILARITY).
 SEQUENCE 275 AA: 31603 MW: 538459F001C59AFA4 CRC64;
 SQ
 Query Match 64.0%; Score 32; DB 1; Length 275;
 Best Local Similarity 50.0%; Pred. No. 39;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GHRPLDKC 8
 ||:||:
 Db 65 GHKPRSRC 72

Search completed: June 16, 2003, 16:03:35
 Job time : 7.93333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 16, 2003, 16:01:29 ; Search time 25.6 Seconds

(without alignments)
64.390 Million cell updates/sec

Title: US-09-424-940a-2
Perfect score: 50
Sequence: 1 GHRPLDKC 8
Scoring table: BL2SUM62
Gapop 10.0 , Gapext 0.5
Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listning first 45 summaries
Database : SPTREMBL_21;*

1:	sp_archaea;*
2:	sp_bacteria;*
3:	sp_fungi;*
4:	sp_invertebrate;*
5:	sp_human;*
6:	sp_invertebrate;*
7:	sp_mammal;*
8:	sp_organelle;*
9:	sp_phage;*
10:	sp_plant;*
11:	sp_rabbit;*
12:	sp_virus;*
13:	sp_vertebrate;*
14:	sp_unclassified;*
15:	sp_rvirus;*
16:	sp_bacteriaph;*
17:	sp_archaeap;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

Q99FX0 PRELIMINARY;
ID Q99FX0; PRT; 377 AA.
AC Q99FX0; DT 01-JUN-2001 (TREMBLrel. 17, Created)
SP Q99FX0; DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
PP Q99FX0; DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE DE Putative regulatory protein E2.
GN GN E2.
OS OS Human papillomavirus type 84..
OC OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus
OX OX NCBI_TaxID=150546;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=21066735; PubMed=11145894;
RA RA Terai M., Burk R.D.;
RT RT "Complete Nucleotide Sequence and Analysis of a Novel Human
Papillomavirus (HPV 84) Genome Cloned by an Overlapping PCR Method.";
RL RL Virology 29:109-115(2001).
RN RN [2]
RP RP SEQUENCE FROM N.A.
RA RA Burk R.D., Terai M.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RL RL EMBL: AF293960; AAK0274.1; -
DR DR HSSP; P17333; LDHM.
DR DR InterPro; IPR000427; E2_C.
DR DR InterPro; IPR001866; E2_N.
PF Pfam: PF00511; E2_C; 1.
DR DR ProDom: PDB00672; E2_N; 1.
DR DR ProDom: PDB00678; E2_N; 1.
SQ SQ SEQUENCE 377 AA; 43001 MW;

Query Match Length DB ID Description
No. Score
1 4.2 84.0 377 1.2 Q99FX0 Q99fx0 human papil
08ww77 homo sapien
Q91fm1 arabidopsis
Q940z1 arabidopsis
Q9ln43 arabidopsis
Q8t326 plasmidum
Q9eg92 porcine ade
Q9eb88 porcine ade
Q8rup6 oryza sativ
Q9ay16 oryza sativ
Q9pfef7 xyliella fas
Q9937 caenorhabdi
Q9si19 arabidopsis
096989 drosophila
Q9va50 drosophila
Q92xy9 rhizobium m

Query Match 84.0%; Score 42; DB 12; Length 377;
Best Local Similarity 75.0%; Pred. No. 2.4;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy Qy 1 GHRPLDKC 8

Db	265	GHRPvSC 272	Qy	1	GHRPLDKC 8
			Db	175	GHRDMDKC 182
RESULT 2					
OBWW77		PRELIMINARY;	PRT;	411	AA.
ID	OBWW77;				
AC	QBWW77;				
DT	01-MAR-2002 (TREMBLrel. 20, Created)				
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DR	Hypothetical 46.9 kDa protein.				
OS	Homo sapiens (Human).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OC	Mammalia; Viridiplantae; Streptophytina; Embryophytina; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBI_TAXID=9606;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	TISSUE=LIVER;				
RA	Strasbourg R., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.				
EMBL	BC020762; AAU20762.1; -				
DR	InterPro; IPR002181; Fibrinogen_C.				
DR	InterPro; IPR010199; Gprotein_alpha.				
DR	Pfam; PF00147; fibrinogen_C; 1.				
DR	Pfam; PF00503; G-alpha; 1.				
DR	SMART; SM00186; FBG; 1.				
DR	SMART; SM00275; G-alpha; 1.				
KW	Hypothetical protein.				
SQ	SEQUENCE 411 AA; 46884 MW; 601B4EA47F60E056 CRC64;				
Query Match	82.0%	Score 41;	DB 4;	Length 411;	
Best Local Similarity	100.0%	Pred. No. 4.1;			
Matches	7	Conservative 0;	-Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GHRPLDK 7			
Db	[1] [1] [1] [1] 45 GHRPLDK 51				
RESULT 3					
Q9LPM1		PRELIMINARY;	PRT;	182	AA.
ID	Q9LPM1;				
AC	Q9LPM1;				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DR	Hypothetical 20.6 kDa protein.				
GN	F211_250.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBI_TAXID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Baner M., Peters S.A., van Staveren M., Dirks W., Stiekema W., Bancroft I., Mewes H.W., Rudd S., Lemke K., Mayer K.F.X.; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.				
RL	NCBI_TAXID=3702;				
RN					
RP	SEQUENCE FROM N.A.				
RA	EU Arabidopsis sequencing project; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AL360314; CAB96671.1; -				
DR	InterPro; IPR000719; Euk_pk kinase.				
DR	ProDom; PD000001; Euk_pk kinase; 1.				
KW	Hypothetical protein.				
SQ	SEQUENCE 182 AA; 20577 MW; F485F31EA802BFBC CRC64;				
Query Match	80.0%	Score 40;	DB 10;	Length 182;	
Best Local Similarity	75.0%	Pred. No. 3.1;			
Matches	6	Conservative 1;	-Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	GHRPLDK 8			
Db	[1] [1] [1] 96 GHKPDDKC 103				
RESULT 4					
Q94OZ1		PRELIMINARY;	PRT;	266	AA.
ID	Q94OZ1;				
AC	Q94OZ1;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	DT1619520/F18014_36.				
DE	Arabidopsis thaliana (Mouse-ear cress).				
OS	Arabidopsis; Viridiplantae; Streptophytina; Embryophytina; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OC	NCBI_TAXID=3702;				
OX	NCBI_TAXID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

RA	Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Ropson C., Khan S., Kim C., Altafai H., Bei Q., Chin C., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howling J., Liu T., Lam B., Lee J., Lenz C., Li J., Liu C., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;	"Genomic sequence for <i>Arabidopsis thaliana</i> BAC F1B014 from chromosome I.",	
RT	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: AC02508; AAF79432; 1..-		
DR	InterPro; IPR002895; PPR.		
DR	Pram; PF01555; PPR; 8.		
DR	TIGRFAMS; TIGR00756; PPR; 7.		
SQ	SEQUENCE: 725 AA; 82535 MW;	921B477745237EFA CRC64;	
Qy	1 GHPLDKC 8	Query Match	Score 78.0%; Score 39; DB 10;
	1 :	Best Local Similarity	Length 725;
Db	555 GHKPDDKC 562	Matches 6;	Pred. No. 17;
		Conservative	Mismatches 1;
			Indels 0;
			Gaps
RESULT 6			
Q8T326	PRELIMINARY;	PRT;	3287 AA.
ID	QBT326		
AC	QBT326;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	PFEMP1 (Fragment).		
GN	TM10VAR.		
OS	Plasmodium falciparum.		
OC	Plasmodium falciparum; Alveolecta; Apicomplexa; Haemosporida; Plasmodium		
NCBI_TAXID=5833;			
OX	[1]		
RN	SEQUENCE FROM N. A.		
RP	STRAIN-TM180;		
RC	MEDLINE=21977235; PubMed=11930336;		
RX	ROWE J.A., KYES S.A., ROGERSON S.J., BANIKER H.A., RAZA A.;		
RA	"Identification of a conserved Plasmodium falciparum var gene implicated in malaria in pregnancy."		
RT	J. Infect. Dis. 185:1207-1211(2002).		
RL	EMBL; AJ420411; CAD20867; 1;		
DR	NON_TER_3287_3287		
FT	SEQUENCE 3287 AA; 383550 MW;	58EF86FC244536 CRC64;	
SQ			
Qy	2 HRPLDKC 8	Query Match	Score 78.0%; Score 39; DB 5;
	1 :	Best Local Similarity	Length 3287;
Db	2872 HRPLDKC 2878	Matches 6;	Pred. No. 68;
		Conservative	Mismatches 0;
			Indels 0;
			Gaps
RESULT 7			
Q9E8G2	PRELIMINARY;	PRT;	50 AA.
ID	Q9E8G2		
AC	Q9E8G2;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	ORF4.		
OS	porcine adenovirus 5.		
OC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.		
OX	[1]		
RN	SEQUENCE FROM N. A.		
RP	STRAIN-HNF-61;		
RC	MEDLINE=20416365; PubMed=10958932;		
RX			

```

RESULTS
RA Tuboly T., Nagy E.; "Sequence analysis and deletion of porcine adenovirus serotype 5 E3
RT region.", Virus Res. 68:109-117(2000).
RT Virus Res. 106:109-117(2000).
RL EMBL: AF186621; AAC10229.1;
DR SEQUENCE 50 AA; MW; D546CCC59A16F417 CRC64;
SQ Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 2 HRPLDKC 8
DB 44 HRPLDTC 50

RESULT 8
Q9EEFB PRELIMINARY; PRT; 50 AA.
ID Q9EEFB
AC
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OREA
OS porcine adenovirus 5.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=45370;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN_HMP-70;
RC MEDLINE=20416365; PubMed=109559982;
RX Tuboly T., Nagy E.;
RA "Sequence analysis and deletion of porcine adenovirus serotype 5 E3
RT region.", Virus Res. 68:109-117(2000).
RL EMBL: AF186622; AAC10234.1;
DR SEQUENCE 50 AA; MW; -02DDECC59A16F3F0 CRC64;
SQ Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 2 HRPLDKC 8
DB 44 HRPLDTC 50

RESULT 9
Q8RDP6 PRELIMINARY; PRT; 401 AA.
ID Q8RDP6
AC
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE P0703B11_15 protein (P0485B12.7 protein).
GN P0703B11_15 ORP45B12.7.
OS Oryza sativa (Japonica cultivar-group)
OC Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryzae.
OX NCBI_TaxID=39847;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN_CV. NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare" (GA3) genomic DNA, chromosome 1, PAC
RA cline:P0703B11_15;
RT Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
STRAIN_CV. NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa (Japonica cultivar-group) genomic DNA, chromosome 1, PAC
RA cline:P0703B11_15;
RT Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

```

RT	clone:P0485B12;	RA	Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	RA	Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
DR	EMBL; AP001302; BAB85296.1; -.	RA	Friga J.S., Franca S.C., Franco M.C., Frohne M., Furian I.R.,
DR	EMBL; AP001348; BAB85477.1; -.	RA	Garnier M., Goldman M.H.S., Gomes S.L., Gruber A.,
SO	SEQUENCE 401 AA; 46131 MW;	RA	HO P.L., Hoineisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
Query Match	Score 38; DB 10; Length 401;	RA	Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Best Local Similarity 75.0%;	Pred. No. 16;	RA	Lemos E.G.M., Lemos M.V.F., Lopes C.R., Machado J.A.,
Matches 6;	Conservative 0; Mismatches 2; Indels 0;	RA	Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Mariano C.L.,
Qy	1 GHRPLDKC 8	RA	Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Db	120 GHSPLQKC 127	RA	Merck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RESULT 10		RA	Nascimento A.L.T.O., Netto L.E.S.,
Q9AY56	PRELIMINARY; PRT; 513 AA.	RA	Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
ID		RA	Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
AC	Q9AY56;	RA	de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
DT	01-JUN-2001 (TREMBLrel. 17, Created)	RA	Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
DT	01-DEC-2001 (TREMBLrel. 17, Last sequence update)	RA	Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	RA	de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Savasaki H.E.,
DE	Hypothetical 57.9 kDa protein.	RA	Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,
GN	OSJNBA0027P10.13.	RA	Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
OS	Oryza sativa (Rice).	RA	Terenzzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
OC	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;	RA	Vallada H., Van Sluys M.A., Verjovska-Almeida S., Vettore A.L.,
OC	Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae;	RA	Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
OX	Ehrhartiidae; Oryzeae; Oryza.	RA	"The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> ,"
RN	[1]	RL	Nature 406:151-159 (2000).
RP	SEQUENCE FROM N.A.	DR	EMBL: AE003913; AAF83512.1.
RC	STRAIN=CV. NIPPONBARE;	DR	KW HYPOTHEtical Protein; Complete proteome.
RA	Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Hsiao J.,	SQ	SQ SEQUENCE 82 AA; 9067 MW; BCDB6C81A85EA7ED CRC64;
RA	Zisman V., Pai G., Bowman C.Y., Fujii C.Y., Vanaken S.E., Craven B.,	Query Match	Query Match Score 74.0%; DB 16; Length 82;
RA	Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L.,	Best Local Similarity 75.0%; Pred. No. 6;	Best Local Similarity 75.0%; Pred. No. 6;
RA	Fraser C.M.;	Mismatches 0;	Mismatches 0;
RT	"Oryza sativa chromosome 10 BAC OSJNBA0027P10 genomic sequence."	Indels 2;	Indels 2;
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	GN	GN C53C9.3.
DR	HYPOTHETICAL protein; EMBL; AAG60187.1; -.	OS	Caenorhabditis elegans
KW	HYPOTHETICAL protein	OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
SO	SEQUENCE 513 AA; 57948 MW; C9EE36E9ABA816BB CRC64;	RN	Rhabditidae; Peloderaiae; Caenorhabditis; NCBI_TAXID=6239;
Query Match	Score 38; DB 10; Length 513;	RN	RN [1]
Best Local Similarity 75.0%;	Pred. No. 20;	RP	SEQUENCE FROM N.A.
Matches 6;	Conservative 0; Mismatches 2;	RC	SPRAIN-BRISTOL N2;
DE	Hypothetical protein Xf0702.	RA	MEDLINE=99065613; PubMed=9851916;
GN	Xylella fastidiosa.	None;	RA
OS	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;	RT	"Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium,"
OC	Xylella.	RT	Science 282:2012-2018 (1998).
NCBI_TaxID=2371;	NCBI_TaxID=2371;	RL	[2]
OX		RN	SEQUENCE FROM N.A.
RN	SEQUENCE FROM N.A.	RC	SPRAIN-BRISTOL N2;
RC	STRAIN=9ASC;	RA	Waterson R.;
RX	MEDLINE=20365717; PubMed=10910347;	RT	"Direct Submission"; to the EMBL/GenBank/DBJ databases.
RA	Simpan A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,	RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RA	Alvarenga R., Alves L.M.C., Araujo J.E., Baia G.S., Baptista C.S.,	DR	EMBL: U28734; AAC52604.1; -.
RA	Barros M.H., Bonacorsi E.D., Bordim S., Bove J.M., Briones M.R.S.,	DR	HS3P; Q54397; IBBL.
RA	Bueno M.R.P., Camargo A.A., Canargo L.E.A., Carraro D.M., Carrer H.,	DR	InterPro; IPR001622; K+channel-pore.
RA	Colaudo N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,	DR	InterPro; IPR003091; K_channel.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champine M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda S.E., Mungall C.J., Nuncio J., Paclob J., Parages V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celinker S., Submitted (AUG 2001) to the EMBL/GenBank/DDJB databases. EMBL; AE03419; AAFA5579; 1; DR EMBL; ALI09630; CAB51681; 1; DR EMBL; AF081540; AA009003; 1; DR EMBL; AY051863; AAKF93285; 1; DR Flybase; FBgn0026143; CD045L; DR InterPro; IPR003874; CD045_lik1. Pfam; PF02724; CDC45; 1; SEQUENCE 575 AA; 65890 MW; A58341D46DEFEE018 CRC64;

Query Match 74.0%; Score 37; DB 5; Length 575; Best Local Similarity 85.7%; Pred. No. 54; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 2 HRPLDK 8 Db 101 HRPLDW 107

RESULT 15
09VA50 ID 09VA50 PRELIMINARY; PRT; 923 AA.
AC Q9VA50;
DT 01-MAY-2000 (TREMBLel. 13, Created)
DT 01-JUN-2000 (TREMBLel. 13, Last sequence update)
DE CG9713 protein.
GN CG9713.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Diopsophilidae; Drosophila;
OX NCBL-TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cainiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Fifeirer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Balliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S., Borrova D., Botchan M.R., Bouck J., Brookstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Dews I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabielian A.F., Garg N.S., Gelbart W.M., Glasser K., Glodck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Keichum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Nobarry C., Morris J., Mostreiki A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner K., Remington R.D.C., Scheier F., Shen H., Shue B.C., Sleden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner E., Venter R., Wang A.H., Wang X., RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zareci J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT The genome sequence of *Drosophila melanogaster*. Science 287:2185-2195 (2000). EMBL; AE00374; AAF5073.1; DR EMBL; FLYBase; FBgn0039793; CG9713; DR InterPro; IPR005123; 2OG-Felli_Oxy; DR PFAM; PF03171; 2OG-Felli_Oxy; 2; SQ SEQUENCE 923 AA; 105446 MW; 7EA45D9BB6E0C929 CRC64;

Query Match 74.0%; Score 37; DB 5; Length 923; Best Local Similarity 85.7%; Pred. No. 54; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 GHRPLDK 7 Db 539 GHRPLEK 545

Search completed: June 16, 2003, 16:04:31
Job time : 26.6 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
protein - Protein search, using SW model
on: June 16, 2003, 16:04:34 ; **Search time** 31.4667 Seconds
(without Alignments)
27.182 Million cell updates/sec
Title: US-09-424-940x-2
perfect score: 50
Sequence: 1 GHRPLDRC 8
Scoring table: BLOSUM62
GapOp 10 0 , Gapext 0.5
DB seq length: 0
Maximum DB seq length: 106915682 residues
searched: 408643 seqs, 106915682 residues
Total number of hits satisfying chosen parameters: 408643
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Fast processing: Minimum Match 0%
Sequence 7, Appl1
Sequence 12, Appl1
Sequence 35105, A
Sequence 46135, A
Sequence 296, App
Sequence 5127, Ap
Sequence 12012, A
Sequence 54, Appl1
Sequence 2, Appl1
Sequence 5, Appl1
Sequence 10, Appl1
Sequence 36299, A
Sequence 465, APP
Sequence 288, APP
Sequence 288, APP
Sequence 33, Appl1
Sequence 158, APP
Sequence 46, APP
Sequence 288, APP
Sequence 110, APP
Sequence 4243, APP
Sequence 179, APP
Sequence 12, Appl1
Sequence 11949, A
Sequence 347, APP

```

; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-4

Query Match 82.0%; Score 41; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
          ||||| |
Db 15 GHRPLDK 21
          ||||| |
```

```

RESULT 3
US-10-131-543-5
; Sequence 5, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; ATTORNEY OR AGENT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic construct
; FEATURE: OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-543-5

Query Match 82.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
          ||||| |
Db 4 GHRPLDK 10
          ||||| |
```

```

RESULT 4
US-10-131-346-5
; Sequence 5, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; ATTORNEY OR AGENT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic construct
; FEATURE: OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-346-5

Query Match 82.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
          ||||| |
Db 4 GHRPLDK 10
          ||||| |
```

```

RESULT 5
US-10-131-546-5
; Sequence 5, Application US/10131546
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; ATTORNEY OR AGENT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic construct
; FEATURE: OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-546-5

Query Match 82.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
          ||||| |
Db 4 GHRPLDK 10
          ||||| |
```

```

RESULT 6
US-10-017-724-6
; Sequence 6, Application US/10017724
; Publication No. US2003099958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeannette
; ATTORNEY OR AGENT: McCarthy, Jeannette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MM1-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic construct
; FEATURE: OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-017-724-6

Query Match 82.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
          ||||| |
Db 4 GHRPLDK 10
          ||||| |
```

```

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-017-724-6

Query Match          82.0%; Score 41; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 9
Db      1 GHRPLDK 7
Db      45 GHRPLDK 51
Length: 20

RESULT 7
US-10-142-935-9
; Sequence 9, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-5

Query Match          72.0%; Score 36; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 5
Db      1 GHRPLDK 6
Db      15 GHRPLDK 20
Length: 20

RESULT 8
US-10-142-935-8
; Sequence 8, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-8

Query Match          72.0%; Score 36; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 6
Db      1 GHRPLDK 6
Length: 15

RESULT 9
US-10-142-935-5
; Sequence 5, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-5

Query Match          72.0%; Score 36; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 5
Db      1 GHRPLDK 6
Db      15 GHRPLDK 20
Length: 20

RESULT 10
US-09-799-875-5
; Sequence 5, Application US/09799875
; Patent No. US20020034780A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Liebermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Human Protein Kinases and Uses
; FILE REFERENCE: 3580/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-5

Query Match          70.0%; Score 35; DB 10; Length 1203;
Best Local Similarity 85.7%; Pred. No. 1.e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO 5
Qy      1 GHRPLDK 7
Db      799 GHRPLSK 805
Length: 1203

RESULT 11
US-08-124-550B-38
; Sequence 38, Application US/08424550B
; Patent No. US2002011947A1
; GENERAL INFORMATION:

```

APPLICANT: JOHN N. SIMONS ; TYPE: PRT
 APPLICANT: TAMI J. PILOT MATIAS ; ORGANISM: Homo sapiens
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT MUEHRHOFF
 APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BUTIK
 APPLICANT: ISA K. MUSHARAF
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 7116
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 ZIP: 60064-5500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version: #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550B
 FILING DATE:
 CLASSIFICATION: 435/35
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 245 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-424 550B-38

Query Match 68.0%; Score 34; DB 8; Length 245;
 Best Local Similarity 75.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 Db 25 GRRPLRKC 32

RESULT 12 US-09-925-300-1483
 ; Sequence 1483, Application US/09925300
 ; Patent No. US2002151671A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: FA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 1483
 ; LENGTH: 370

Query Match 68.0%; Score 34; DB 10; Length 370;
 Best Local Similarity 71.4%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HRPDLDKC 8
 Db 84 HMPDLDEC 90

RESULT 13 US-09-801-368-348
 ; Sequence 348, Application US/09801368
 ; Patent No. US2002128250A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Busby, Robert
 ; APPLICANT: Cali, Brian
 ; APPLICANT: Hecht, Peter
 ; APPLICANT: Holtzman, Doug
 ; APPLICANT: Madden, Kevin
 ; APPLICANT: Maxon, Mary
 ; APPLICANT: Milne, Todd
 ; APPLICANT: No, US20020128250A1man, Thea
 ; APPLICANT: Royer, John
 ; APPLICANT: Salama, Sofie
 ; APPLICANT: Sherman, Amir
 ; APPLICANT: Silva, Jeff
 ; APPLICANT: Summers, Eric
 ; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fung
 ; FILE REFERENCE: 109272_147
 ; CURRENT APPLICATION NUMBER: US/09/801-368
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 09/1487,558
 ; PRIOR FILING DATE: 2000-01-19
 ; PRIOR APPLICATION NUMBER: US 60/160,587
 ; PRIOR FILING DATE: 1999-10-20
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 348
 ; LENGTH: 785
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-801-368-348

Query Match 64.0%; Score 32; DB 10; Length 785;
 Best Local Similarity 62.5%; Pred. No. 4,1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 Db 590 GERPLKKC 597

RESULT 14 US-10-072-094-9
 ; Sequence 9, Application US/10072094
 ; Publication No. US2003025538A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JACKSON, DONALD
 ; APPLICANT: LORENZI, MATTHEW
 ; APPLICANT: ATTAR, RICARDO
 ; APPLICANT: GOTTARDIS, MARCO
 ; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
 ; FILE REFERENCE: 3053-4145US1
 ; CURRENT APPLICATION NUMBER: US/10/072,094
 ; CURRENT FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: 60/298,296
 ; PRIOR FILING DATE: 2001-06-14
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO: 9
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-094-9

Query Match          64.0%; Score 32; DB 9; Length 855;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GHRPLDK 7
        ||||| :
Db      437 GHRPLSR 443

```

```

RESULT 15
US-09-817-913-13
Sequence 13, Application US/09817913
; Patent No. US20030061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuwemei
; APPLICANT: Bonneil, Claire
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-817-913-13

```

```

Query Match          64.0%; Score 32; DB 10; Length 855;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GHRPLDK 7
        ||||| :
Db      437 GHRPLSR 443

```

Search completed: June 16, 2003, 16:16:37
Job time : 32.4667 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2003, 16:00:28 ; Search time 28 Seconds

(without alignments)
33.313 Million cell updates/sec

Title: US-09-424-940A-1
Perfect score: 41

Sequence: 1 GHRPLDK 7

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

RESULT 1

AAP71314

ID AAP71314 standard; peptide; 7 AA.

XX

AC AAP71314;

XX

DT 03-OCT-2002 (updated)

DT 19-JUN-1991 (first entry)

XX DE Sequence of fibrin immunogen for the prepn. of monoclonal antibodies (Mabs).

XX KW Fibrin-specific monoclonal antibody; screening.

XX OS Homo sapiens.

XX FT Key Misc-difference /label= Lys-OH

XX FH Location/Qualifiers

XX FT

XX PN WO87/06263-A.

XX PD 22-OCT-1987.

XX PF 14-APR-1987; 87WO-US00862.

XX PR 14-APR-1986; 86US-0851514.

XX PA (GENO-) GEN HOSPITAL CORP.

XX PA (GENO-) GEN HOSPITAL CORP.

XX PI Matsueda GR, Haber E;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	41	100.0	7	8	AAP71314		Sequence of fibrin peptide antigenic Beta-peptide used
2	41	100.0	7	11	AAR05558		Fibrin-specific ep Human fibrin beta-Synthetic beta-pep
3	41	100.0	7	15	AARE3269		Fibrin-specific ep Residues 45-54 of Fibrinogen A-alpha
4	41	100.0	7	15	AAR05792		
5	41	100.0	8	9	AAPB1686		
6	41	100.0	8	14	AAR44837		
7	41	100.0	8	15	AAR03270		
8	41	100.0	8	15	AARE5793		
9	41	100.0	9	22	ABBT6979		
10	41	100.0	10	16	AAN11931		

DR WPI; 1987-30685/43.
 XX Screening of fibrin-specific monoclonal antibodies - by contact
 PT with immobilised crosslinked fibrin clot and screening with
 PT detectable labelling step
 XX PS Disclosure; Page 7; 41pp; English.
 CC The MABS are specific to fibrin without fibrinogen cross-reactivity.
 CC They have increased binding to in vitro and in vivo thrombi. The
 CC MABS can be used in immunoassays for fibrin in the presence of
 CC fibrinogen or other proteins. They can be used as immunoaffinity
 CC ligands for the purification of fibrin.
 CC (Updated on 03-OCT-2002 to add missing OS field.)
 XX SQ Sequence 7 AA;

Query Match 100.0%; Score: 41; DB: 8; Length: 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 2
 ID AAR05558 standard; peptide: 7 AA.
 XX AC AAR05558;
 XX DT 11-OCT-1990 (first entry)
 DE Peptide antigenic to fibrin.
 XX KW fibrin; fibrinogen; thrombi; immunoaffinity.
 XX OS Synthetic.

XX FH Key-Location/Qualifiers
 FT Misc-difference 2
 FT /label=His or Pro
 FT Misc-difference 4
 FT /label=Pro or Val
 FT Misc-difference 5
 FT /label=Leu or Val
 FT Misc-difference 6
 FT /label=Asp or Glu
 FT Misc-difference 7
 FT /label=Lys or Arg
 XX PS US4027916-A.
 XX PD 22-MAY-1990.
 XX PF 30-JAN-1986; 86US-0824228.
 XX PR 23-APR-1984; 84US-060155.
 XX PR 30-JAN-1986; 86US-0824228.
 PA (GEHO-) GEN HOSPITAL CORP.
 XX PI Matsueda GR, Haber E, Hui K;
 XX DR WPI; 1990-185723/24.

XX Fibrin-specific monoclonal antibodies - lacking fibrinogen cross-reactivity, obt'd. using peptide(s)
 PT comprising fibrin specific epitopic sequences.
 XX Claim 1; Page 17; 12pp; English.
 XX PS

CC Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be
 CC raised without cross-reactivity to fibrinogen. They are
 CC particularly useful in detection of fibrin and thrombi.
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score: 41; DB: 11; Length: 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 3

AAR63269 standard; peptide: 7 AA.
 ID AAR63269
 XX AC AAR63269;
 XX DT 21-JUL-1995 (first entry)
 DE Beta-peptide used to raise monoclonal antibody 59D8.

XX Beta-peptide used to raise monoclonal antibody 59D8.

XX Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
 KW Hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
 KW coronary stent implantation; adjunctive therapy; fibrinogen;
 KW haemorrhage.
 XX Synthetic.

XX PN WO9425491-A.

XX PD 10-NOV-1994.

XX PF 03-MAY-1994; 94WO-US04881.
 XX PR 03-MAY-1993; 93US-0058699.
 XX PA (HARD) HARVARD COLLEGE.
 XX PA (UYEM-) UNIV ENORY.
 XX PI Bode C, Haber E, Runge M;
 XX DR 1994-358195/44.

XX Fibrin-binding antibody linked to thrombin inhibitor - useful for
 PT preventing blood coagulation by specifically targetting inhibitor
 PT to site of thrombin activity
 XX PS Example 1; Page 13; 53pp; English.
 XX This sequence represents beta-peptide which was used to raise the
 CC monoclonal antibody 59D8. The antibody binds fibrin and may be used
 CC in the chimeric molecule of the invention. The chimeric molecule
 CC further comprises a thrombin inhibitor linked to the fibrin-binding
 CC antibody through a covalent linkage. The chimeric molecule allows
 CC fibrin-specific antibody targeting of hirudin and other thrombin
 CC inhibitors, which is more potent than thrombin on its own. The epitope
 CC to which 59D8 binds becomes available only after thrombin cleaves
 CC fibrinopeptide B. The chimeric protein may be used for preventing
 CC coagulation of the blood. Anti-thrombin targeting can be esp. useful
 CC in highly thrombogenic situations such as coronary stent implantation
 CC and can be used as an adjunctive therapy with highly selective
 CC thrombolytic agents. The thrombin inhibitor is localised to sites
 CC of thrombin activity by the antibody which binds to thrombin but does
 CC not cross react with uncleaved fibrinogen. The selectivity of
 CC inhibition allows the total amount of thrombin inhibitor used to be
 CC substantially reduced, resulting in a reduced potential for generalised
 CC haemorrhaging.
 XX SQ Sequence 7 AA;

PS Example 1; Page 14; 38pp; Japanese.
 XX Human fibrin beta-chain peptides A and B were synthesised and coupled
 CC to BSA for injection into mice. The peptides were used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
 CC are used in the production of bispecific monoclonal antibodies
 CC which also recognise truncated tPA muteins lacking the finger, EGF and
 CC Kringle 1 domains.
 XX Sequence 8 AA;

Query Match 100.0%; Score 41; DB 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7

Db 1 GHRPLDK 7

RESULT 7
 ID AAR63270 standard; Peptide; 8 AA.

XX AC AAR63270;

XX DT 21-JUL-1995 (first entry)

DE Synthetic beta-peptide used to raise monoclonal antibody 59D8.

XX Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;

KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;

KW coronary stent implantation; adjunctive therapy; fibrinogen;

KW haemorrhage.

XX Synthetic.

OS WO9425491-A.

XX PN

PD 10-NOV-1994.

XX PF 03-MAY-1994; 94WO-US04881.

XX PR 03-MAY-1993; 93US-0058699.

XX (HARD) HARVARD COLLEGE.

PA (UTEM-) UNIV EMORY.

XX PI Bode C, Haber E, Runge M;

XX DR 1994-358195/44.

XX PT Fibrin-binding antibody linked to thrombin inhibitor - useful for

PT preventing blood coagulation by specifically targetting inhibitor

PT to site of thrombin activity

XX PS Example 1; Page 14; 53pp; English.

XX CC This sequence represents a synthetic beta-peptide which was used to

CC immunopurify the monoclonal antibody 59D8 which was raised against

CC a beta-peptide (see also AAR63269). The antibody binds fibrin and may be

CC used in the chimeric molecule of the invention. The chimeric molecule

CC further comprises a thrombin inhibitor linked to the fibrin-binding

CC antibody through a covalent linkage. The chimeric molecule allows

CC fibrin-specific antibody targetting of hirudin and other thrombin

CC inhibitors, which is more potent than thrombin on its own. The epitope

CC to which 59D8 binds becomes available only after thrombin cleaves

CC fibrinopeptide B. The chimeric protein may be used for preventing

CC coagulation of the blood. Anti-thrombin targetting can be esp. useful

CC in highly thrombotic situations such as coronary stent implantation

CC and can be used as an adjunctive therapy with highly selective

CC thrombolytic agents. The thrombin inhibitor is localised to sites

CC of thrombin activity by the antibody which binds to thrombin but does

CC not cross react with uncleaved fibrinogen. The selectivity of

CC inhibition allows the total amount of thrombin inhibitor used to be

CC substantially reduced, resulting in a reduced potential for generalised

CC haemorrhaging.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 41; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 ID AAR65793 standard; peptide; 8 AA.

XX AC AAR65793;

XX DT 26-JUN-1995 (first entry)

XX DE Fibrin-specific epitopic peptide.

XX FW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;

KW anti-fibrin-specific monoclonal antibodies.

XX Synthetic.

OS OS

XX FH Key Location/Qualifiers

XX FT Misc-difference 8 /note= "May be absent and if present

FT may be bonded to keyhole limpet
FT hemocyanin."

XX PN US5357042-A.

XX PD 18-OCT-1994.

XX PF 23-APR-1984; 84US-0603155.

XX PR 23-APR-1984; 84US-0603155.

XX PR 30-JAN-1986; 86US-0824228.

XX PR 22-DEC-1989; 89US-0454554.

XX PR 24-AUG-1992; 92US-0932729.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PI Haber E, Hui K, Matsueda GR;

XX DR WPI: 1994-332411/41.

XX PT Synthetic epitopic peptide(s) of variable length - capable of

PT eliciting fibrin specific antibodies free of fibrinogen

PT cross reactivity.

XX XX Claim 3; Column 18; 12pp; English.

XX XX CC AAR65789-R65794 are synthetic peptides comprising fibrin-specific

CC epitopic sequences, they can be used to prepare hybridoma cell

CC lines, which produce antifibrin-specific monoclonal antibodies

CC substantially devoid of fibrinogen cross-reactivity. These

CC antibodies are useful in the in vivo and in vitro detection

CC of thrombi and fibrin deposits.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 9
ID ABB76979 standard; peptide; 9 AA.
XX AC ABB76979;
XX DT 22-JUL-2002 (first entry)
XX DE Residues 45-54 of human fibrinogen beta chain precursor.
XX KW Anti-arthritis; anti-inflammatory; fibrin; rheumatoid polyarthritis;
KW human; fibrinogen beta chain.
XX OS Homo sapiens.
PN FR2795735-A1.

XX PD 05-JAN-2001.
XX PF 01-JUL-1999; 99FR-0008470.
XX PR 01-JUL-1999; 99FR-0008470.
XX PA (UTR0-) UNIV TOULOUSE SABATIER PAUL.
XX PI Serre G, Sebbag M;
XX DR WPI: 2001-114394/13.
XX PT New citrulline-containing polypeptide from fibrin, useful for diagnosis
PT and treatment of rheumatoid polyarthritis.
XX PS Example 1; Page 12; 23pp; French.
XX CC The present invention relates to a citrulline (Cit) containing
CC polypeptide derived from all or part of the alpha- or beta-chains of
CC fibrin by substitution of at least one arginine residue by Cit. The Cit
CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
CC therapeutically for neutralising the RP-associated autoimmune response.
CC The present sequence is a fragment (residues 45-54) of the human
CC fibrinogen beta chain precursor, which was used in an example from the
CC invention.
XX Sequence 9 AA;

SQ Query Match 100.0%; Score 41; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 10
ID AAW11931 standard; peptide; 10 AA.
XX AC AAW11931;
XX DT 02-APR-1997 (first entry)
XX DE Fibrinogen A-alpha-chain residues 17-26.
XX KW Monoclonal; antibody; human; soluble; fibrin; immunoassay; diagnosis;
KW urea-treated; des-NABB; A-alpha-chain; immunoassay; fibrinogen;
KW disseminated intravascular coagulation.

XX OS Homo sapiens.
PN WO9512617-A1.
XX PD 11-MAY-1995.
XX PF 01-NOV-1994; 94WO-JP01844.
XX PR 02-NOV-1993; 93JP-0297325.
XX PA (IATR) IATRON LAB INC.
XX PI Inuzuka K, Ito Y, Kohno I, Soe G;
XX DR WPI: 1995-206667/27.
XX PT Monoclonal antibody reactive with soluble human fibrin - but not
PT with fibrinogen, is useful for fibrin immunoassay in plasma
PT specimens.
XX Example 3; Page 15; 32pp; Japanese.
PS XX
CC A novel monoclonal antibody (Mab) reacts with human soluble fibrin,
CC but not with human fibrinogen. Specifically when the Mab reacts
CC with urea-treated desAABB fibrin the reaction is not inhibited by
CC peptides corresponding to fibrinogen A-alpha-chain residues 17-26
CC (AAW11931), B-beta-chain residues 15-24 (AAW11932) or gamma-chain
CC residues 312-324 (AAW11933). The Mab is useful in immunoassays for
CC soluble fibrin in plasma samples (e.g., by sandwich immunoassay),
CC particularly for the diagnosis of pathological conditions such as
CC disseminated intravascular coagulation.
XX Sequence 10 AA;
SQ Query Match 100.0%; Score 41; DB 16;
Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 11
ID AAR28629 standard; peptide; 12 AA.
XX AC AAR28629;
XX DR 22-MAR-1993 (first entry)
XX DE N-terminal human fibrin peptide.
XX PN EP513778-A.
XX PD 19-NOV-1992.
XX PF 14-MAY-1992; 92EP-0108134.
XX PR 17-MAY-1991; 91JP-0112874.
XX PR 13-MAR-1992; 92JP-0055025.
XX PA (TAKE) TAKEDA CHEM IND LTD.
XX PI Iwasa S, Kurokawa T, Watanabe A;

DR WPI; 1992-383677/47.
 XX Bi:specific antibody useful for treating thrombotic obstructive
 PT diseases e.g. cardiac infarction - comprises antigenic substance antibody
 PT antibody variable region and anti-thrombolytic substance antibody
 PT variable region with no heavy chain constant region domains 2 and
 PT 3
 XX Disclosure; Page 3; 30pp; English.

PS XX This sequence represents an N-terminal peptide of human fibrin. It
 CC was used in the production of bispecific monoclonal antibodies which
 CC are specific for fibrin, but do not bind fibrinogen, and are
 CC specific for anti-thrombolytic substance. The compsn. contg. these
 CC Abs lacks the side effects of prior art Ab targetted thrombolytic
 CC agents and has enhanced thrombolytic activity.

XX Sequence 12 AA;

Query Match 100.0%; Score 41; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7

RESULT 12
 AAR44829 ID AAR44829 standard; peptide; 12 AA.
 XX AC AAR44829;
 XX DT 20-JUN-1994 (first entry)
 DE Human fibrin beta-chain N-terminal peptide (1-11)-Cys.
 XX Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH 1.11
 FT /note= "human fibrin beta-chain residues 1-11"
 FT Modified-site 12
 FT /note= "BSA carrier is attached to Cys"
 PN JP05304992-A.
 XX PD 19-NOV-1993.
 XX PF 17-JUN-1992; 92JP-0158301.
 PR 20-JUN-1991; 91JP-0148936.
 PA (TAKE) TAKEDA CHEM IND LTD.
 DR WPI; 1993-408334/51.
 XX Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX Disclosure; Page 9; 38pp; Japanese.

PS XX Human fibrin beta-chain N-terminal peptide (1-11)-Cys was
 CC synthesised and coupled to BSA for injection into mice. The peptide
 CC was used to raise antibodies to human fibrin. Monoclonal antibodies
 CC specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins

CC Lacking the finger, EGF and Kringle 1 domains.
 XX Sequence 12 AA;
 Query Match 100.0%; Score 41; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7

RESULT 13
 AAR44838 ID AAR44838 standard; peptide; 12 AA.
 XX AC AAR44838;
 XX DT 20-JUN-1994 (first entry)
 DE Human fibrin beta-chain peptide B.
 XX Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 XX Synthetic.
 XX PS JP05304992-A.
 XX PD 19-NOV-1993.
 XX PF 17-JUN-1992; 92JP-0158301.
 XX PR 20-JUN-1991; 91JP-0148936.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX DR WPI; 1993-408334/51.
 XX PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX PS Example 1; Page 14; 38pp; Japanese.
 XX Human fibrin beta-chain peptides A and B were synthesised and coupled
 CC to BSA for injection into mice. The peptides were used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
 CC are used in the production of bispecific monoclonal antibodies
 CC which also recognise truncated tPA muteins lacking the finger, EGF and
 CC Kringle 1 domains.
 XX SQ Sequence 12 AA;

Query Match 100.0%; Score 41; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 6 GHRPLDK 12

RESULT 14
 AAR44830 ID AAR44830 standard; peptide; 16 AA.
 XX AC AAR44830;
 XX DT 20-JUN-1994 (first entry)

DE Human fibrin beta-chain internal peptide fragment.
 XX
 KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolytic
 KW agent; bispecific antibody.
 OS Synthetic.
 XX
 PN JP05304992-A.
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKEDA CHEM IND LTD.
 XX
 PS WPI; 1993-408334/51.
 XX
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX Disclosure; Page 9; 38pp; Japanese.
 XX
 CC Human fibrin internal peptide fragment was identified as a
 CC candidate immunogen to raise antibodies to human fibrin. Monoclonal
 CC antibodies specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins
 CC lacking the finger, EGF and Kringle 1 domains.
 XX Sequence 16 AA:
 CC Query Match Score 41; DB 14; Length 16;
 CC Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 GHRPLDK 7
 CC | | | | |
 CC .Db 1 GHRPLDK 7
 CC | | | | |
 CC 6 GHRPLDK 12

RESULT 15
 AAR40010
 ID AAR40010 standard; peptide; 28 AA.
 XX
 AC AAR40010;
 XX
 DT 23-MAY-1994 (first entry)
 XX
 DE Scintigraph imaging agent specific binding peptide.
 XX
 KW Reagent; site imaging; technetium-99M labelled; peptide.
 XX
 OS Synthetic.
 XX
 FN WO9321962-A.
 XX
 PD 11-NOV-1993.
 XX
 PF 19-APR-1993; 93WO-US03687.
 XX
 PR 30-APR-1992; 92US-0871282.
 XX
 PA (DIA-T) DIATECH INC.
 XX
 PI Buttram S, Civitello ER, Dean RT, Lister-James J, McBride W;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2003, 16:01:49 ; Search time 11.6667 Seconds
(without alignments)
57.681 Million cell updates/sec

Title: US-09-424-940A-1
Perfect score: 41
Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database : PIR_73;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	31	A05297	fibrinogen beta ch
2	41	100.0	491	1 FGHUB	fibrinogen beta ch
3	36	87.8	201	2 C95399	probable transcript
4	36	87.8	468	1 FGBOB	fibrinogen beta ch
5	36	87.8	1490	2 T47840	multi resistance P
6	35	85.4	463	2 A38463	fibrinogen beta ch
7	34	82.9	673	2 T40817	zinc finger protein
8	34	82.9	795	2 A84608	hypothetical prote
9	33	80.5	225	2 A75550	MutY/nudix family
10	33	80.5	1058	2 D82654	ankyrin-like prote
11	32	78.0	423	2 T20233	hypothetical prote
12	32	78.0	476	2 E87040	acyl-CoA synthase
13	32	78.0	485	2 F70464	hypothetical prote
14	32	78.0	611	2 D84423	probable WD-40 rep
15	32	78.0	878	2 T17245	hypothetical prote
16	31	75.6	42	2 B92087	myelin basic prote
17	31	75.6	169	1 MBBOB	hypothetical prote
18	31	75.6	176	2 F72465	protein T17H7.16 [
19	31	75.6	215	2 D86434	pyroglutamyl-pepti
20	31	75.6	215	2 S23432	hypothetical prote
21	31	75.6	225	2 T25957	probable APP-bindi
22	31	75.6	228	2 D83071	hypothetical prote
23	31	75.6	250	2 T46417	hypothetical prote
24	31	75.6	309	2 T19389	hypothetical prote
25	31	75.6	343	2 E71149	hypothetical prote
26	31	75.6	344	2 H87110	hypothetical prote
27	31	75.6	345	2 D96011	probable oxidoredu
28	31	75.6	374	2 S77072	queine tRNA-ribos
29	31	75.6	424	2 C69077	thiamin biosynthes

ALIGNMENTS

RESULT 1
A05297
fibrinogen beta chain - Dog (fragment)
C; Species: Canis lupus familiaris (dog)
C; Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996
C; Accession: B94308; A03123; A37512; B37512; D03118
R; Birken, S.; Wilner, G.D.; Caufield, R.E.
Thromb. Res. 7, 599-510, 1975
A; Title: Studies of the structure of canine fibrinogen.
A; Reference number: A94308; MUID:76081726; PMID:1198547
A; Accession: B94308
A; Molecule type: protein
A; Residues: 1-31 <BLO>
R; Blomhaeck, B.; Blomhaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 22, 1339-1346, 1968
A; Reference number: A37512; MUID:69066367; PMID:5727635
A; Accession: A37512
A; Molecule type: protein
A; Residues: 1-19 <KRA>
C; Superfamily: fibrinogen beta/gamma homology; fibrinogen d1
C; Keywords: blood coagulation; liver; plasma; sulfoprotein
C; 1-19/Product: fibrinopeptide B #status experimental <ART>
F; 2/Binding site: sulfate (Tyr) (covalent) #status experimental
F; 3/Banding site: sulfate (Tyr) (covalent) #status experimental

Query Match 100.0%; Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.054
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
Db 20 GHRPLDK 26

RESULT 2
FGHUB
fibrinogen beta chain precursor [validated] - human
N; Alternate names: coagulation factor I
N; Contains: fibrinopeptide B
C; Species: Homo sapiens (man)
C; Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000
C; Accession: B41568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121
R; Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A; Title: Nucleotide sequences of the three genes coding for human fibrinogen.

A; Reference number: A43568; MUID: 91344740; PMID: 2102623
 A; Accession: BA3568
 A; Molecule type: DNA
 A; Residues: 9-191, P, 193-491 <CHD>
 R; Chung, D.W.; Que, B.G.; Rixon, M.W.; Nace Jr., M.; Davie, E.W.
 Biochemistry 22, 3244-3250, 1983
 A; Reference number: A90469; MUID: 83283433; PMID: 6588356
 A; Accession: A90469
 A; Molecule type: protein
 A; Residues: 1-38 <CH1>
 A; Accession: B90469
 A; Molecule type: mRNA
 A; Residues: 9-191, A, 193-491
 A; Cross-references: GB:J00129; NID:9182429; PID:AAA52429_1; PID:9182430
 R; Huber, R.; Salmon, J.; Courtois, G.; Laurent, M.; Marguerie, G.
 Nucleic Acids Res. 15, 1615-1625, 1987
 A; Title: Characterisation of the 5'-flanking region for the human fibrinogen beta gene.
 A; Reference number: 137389; MUID: 87146483; PMID: 3029722
 A; Accession: 137389
 A; Status: translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-38 <HBD>
 A; Cross-references: EMBL:X05018; NID:g31400; PID:931401
 R; Henschen, A.; Lottspeich, F.; Southan, C.; Topf-Petersen, E.
 Proteins of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
 A; Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural
 A; Reference number: A94433
 A; Contents: carbohydrate binding
 A; Accession: A94433
 A; Molecule type: protein
 A; Residues: 31-137, 'QS', '140-144,'QF', '147-491 <HEN>
 R; Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
 Biochemistry 18, 68-76, 1979
 A; Title: Amino acid sequence of the beta chain of human fibrinogen.
 A; Reference number: A90437; MUID: 79124640; PMID: 420779
 A; Accession: A90437
 A; Molecule type: protein
 A; Residues: 31-144, 'QF', '147-231, 'D', '233-330, 'E', '332-491 <WAT>
 R; Blomback, B.; Hessell, B.; Hegg, D.
 Thromb. Res. 8, 639-658, 1976
 A; Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
 A; Reference number: A94309; MUID: 76225080; PMID: 936108
 A; Contents: disulfide bonds
 A; Accession: A94309
 A; Molecule type: protein
 A; Residues: 31-112, E', '14-137, 'QS', '140-144,'QF', '147-148 <BLD>
 R; Kunlith, S.T.; Carilli, C.; Lau, K.; Procter, A.A.; Nayla-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A; Title: Identification of proteins associated with apolipoprotein A-I-containing lipop
 A; Reference number: A54223; MUID: 94162201; PMID: 8117655
 A; Accession: G54223
 A; Molecule type: protein
 A; Residues: 164-174 <KUN>
 A; Note: Identification of tryptic peptides from high-density lipoproteins
 R; Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983
 A; Title: Covalent structure of fibrinogen
 A; Reference number: A91249; MUID: 77245939; PMID: 6575689
 A; Contents: annotation; review, disulfide bonds
 R; Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
 Eur. J. Biochem. 77, 595-610, 1977
 A; Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983
 A; Reference number: A91249; MUID: 77245939; PMID: 6575689
 A; Contents: annotation; disulfide bonds
 R; Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
 in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S.; Ottessen, M., Eds.
 A; Title: The structures of fibrinogen and fibrin.
 A; Reference number: A94437
 A; Contents: annotation; disulfide bonds
 R; Doolittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A; Title: Fibrinogen and fibrin.

A; Reference number: A90041; MUID: 84305751; PMID: 6383194
 A; Contents: annotation; review, EM structure, Polymerization, ligands
 R; Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
 Ann. N. Y. Acad. Sci. 408, 449-456, 1983
 A; Title: Cloning of fibrinogen genes and their cDNA.
 A; Reference number: A90038; MUID: 83254384; PMID: 6575700
 A; Contents: annotation
 R; Kirschbaum, N.B.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13669-13676, 1990
 A; Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COC
 A; Reference number: A71117; MUID: 90337977; PMID: 2143188
 A; Contents: annotation; hemolin cleavage site
 A; Note: hemolin, a protease from Haementeria ghilianii, the giant South American leech
 C; Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleavage sites responsible for the formation of the soft clot.
 C; Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-ester)
 C; Comment: All fibrinogen chains are synthesized in the liver.
 C; Genes:
 A; Gene: GDB:FGB
 A; Cross references: GDB:119130; OMIM:134830
 A; Map position: 4q28-q28
 A; Map position: A71117; MUID: 90337977; PMID: 2143188
 A; Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
 C; Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PI 1) and two sets of beta (see PI 2). The fibrinogen molecule is a hexamer containing two sets of alpha (see PI 1) and two sets of beta (see PI 2). The fibrinogen molecule is a hexamer containing two sets of alpha (see PI 1) and two sets of beta (see PI 2). The fibrinogen molecule is a hexamer containing two sets of alpha (see PI 1) and two sets of beta (see PI 2).
 C; Function:
 A; Description: fibrinogen cleaved by thrombin yields monomers that are polymerized i
 A; Pathway: blood coagulation
 C; Superfamily: fibrinogen beta chain; fibrinogen homology; fibrinogen dis
 C; Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglobutami
 F: 1-30/Domain: (or 4-30 or 15-30) signal sequence #status Predicted <SIG>
 F: 31-491/Product: fibrinogen beta chain #status experimental <MAT>
 F: 31-491/Product: fibrinopeptide B #status experimental <APF>
 F: 31-44/Product: fibrinopeptide B #status experimental <APB>
 F: 45-47/Region: polymerization site
 F: 238-487/Domain: fibrinogen beta chain #status experimental <FGB>
 F: 238-487/Domain: fibrinogen beta/gamma homology <FBG>
 F: 31-70/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper
 F: 44-45/Cleavage site: Arg Gly (thrombin) #status experimental
 F: 95/Disulfide bonds: interchain (to alpha-55) #status experimental
 F: 106/Disulfide bonds: interchain (to alpha-68) #status experimental
 F: 110/Disulfide bonds: interchain (to gamma-45) #status experimental
 F: 223/Disulfide bonds: interchain (to alpha-184) #status experimental
 F: 227/Disulfide bonds: interchain (to gamma-161) #status experimental
 F: 231-241-270 424-437/Disulfide bonds: #status experimental
 F: 394/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 100.0%; Score 41; DB 1; Length 491;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 C95399
 Probable transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) m
 C; Species: Sinorhizobium meliloti
 C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C; Accession: C95399
 R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler, F.;
 ; Kallman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh,
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium mel
 A; Reference number: A95262; MUID: 21396509; PMID: 11481432
 A; Accession: C95399
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-201 <KUR>
 A; Cross-references: GB:AE006469; PID:AAK65757.1; PMID:g14524255; GSPDB:GN00165

A; Experimental source: strain 1021, megaplasmid pSYMA
 B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebaute, P.; Vandenbrou, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A; Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A; Reference number: A96039; PMID:21368234; PMID:11474104
 A; Contents: annotation
 C; Genetics:
 A; Gene: SME2008
 A; Genome: Plasmid

Query Match
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLD 6
 Db 175 GHRPLD 180

RESULT 4

FGBOB
 Fibronogen beta chain - bovine
 N; Contains: fibronopeptide B
 C; Species: Bos primigenius taurus (cattle)
 C; Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
 C; Accession: A03122; B03117; B37507; A37513; S02443
 R; Blomback, B.; Doolittle, R.F.
 Acta Chem. Scand. 17, 1816-1819, 1963
 A; Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
 A; Reference number: A03122
 A; Accession: A03122
 - A; Molecule type: protein
 A; Residues: 1-4 <BLO>
 R; Sjöquist, J.; Blomback, B.; Wallen, P.
 Ark. Kemi 16, 425-436, 1960
 A; Title: Amino acid sequence of bovine fibrinopeptides.
 A; Reference number: A03117
 A; Accession: B03117
 A; Molecule type: protein
 A; Residues: 5-21 <SJO>
 R; Martineau, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A; Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
 A; Reference number: A37507; PMID:79164394; PMID:434821

A; Molecule type: protein
 A; Residues: 22-53 <MAP>
 R; Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
 A; Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
 A; Reference number: A37513; MUID:81199473; PMID:6262803
 A; Accession: A37513
 A; Molecule type: mRNA
 A; Residues: 44-68 <CHD>
 R; Medved, L.V.; Plattonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
 FEBS Lett. 232, 56-60, 1988
 A; Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
 A; Reference number: S02443; MUID:88211875; PMID:2966748
 A; Accession: S02443
 A; Molecule type: protein
 A; Residues: 373-374 <HED>
 C; Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
 C; Superfamily: fibrinogen is a hexamer containing two sets of three non-identical chains (alpha
 C; Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein
 F; 16-164/Domain: fibrinogen disulfide ring homology <FBG>
 F; 215-164/Domain: fibrinogen beta/gamma homology <FBG>
 F; 1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
 F; 6/Binding site: sulfate (Tyr) (covalent) #status experimental

F; 21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
 F; 371/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match
 Best Local Similarity 87.8%; Score 36; DB 1; Length 468;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GHRPLD 7
 Db 22 GHRPLD 28

RESULT 5

T4740
 multi resistance protein homolog - Arabidopsis thaliana
 N; Alternative names: protein T209-140
 C; Species: Arabidopsis thaliana (mouse-ear cress)
 C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
 C; Accession: T47840
 R; Nyakatura, G.; Furtmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner,
 submitted to the Protein Sequence Database, February 2000
 A; Reference number: Z24475
 A; Accession: T47840
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-1490 <NYA>
 A; Cross-references: EMBL AL138658
 A; Experimental source: cultivar Columbia; BAC clone T209
 C; Genetics:
 A; Map position: 3
 A; Intron: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3;
 A; Note: T209-140
 C; Superfamily: human multidrug resistance protein CMQR2; ATP-binding cassette homo
 Query Match
 Best Local Similarity 87.8%; Score 36; DB 2; Length 1490;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GHRPLD 6
 Db 1226 GHRPLD 1231

RESULT 6

A38463
 fibrinogen beta chain - chicken (fragment)
 C; Species: Gallus gallus (chicken)
 C; Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
 C; Accession: A38463
 R; Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
 Biochemistry 30, 3290-3294, 1991
 A; Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
 A; Reference number: A38463; MUID:91182745; PMID:20092666
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-463 <WEI>
 A; Cross-references: GB:MB8514; NID:9211779; PID:AAA48770.1;
 C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen d1
 F; 73-202/Domain: fibrinogen disulfide ring homology <PDR>
 F; 212-460/Domain: fibrinogen beta/gamma homology <FBG>
 Query Match
 Best Local Similarity 100.0%; Score 35; DB 2; Length 463;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 HRLDK 7
 Db 19 HRLDK 24

RESULT 7

A;Cross-references: EMBL:Z75533; PIDN:CAA99815.1; GSPDB:GN00019; CESP:C54G4 .2
 A;Experimental source: clone C54G4
 C;Genetics:
 A;Gene: CESP :C54G4 .2
 A;Nap position: 1
 A;Introns: 76/3; 172/3; 272/2; 312/1; 367/3
 C;Superfamily: Caenorhabditis elegans hypothetical protein C54G4 .2
 Query Match 78 .0%; Score 32; DB 2; Length 423;
 Best Local Similarity 83 .3%; Pred. No. 72;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 HRPDK 7
 Db 197 HRPDK 202

Db 18 GDRPLDK 24

RESULT 14
 D84423
 probable WD-40-repeat protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: D84423
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Talle euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; PMID:10617197
 A;Accession: D84423
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-611 <STO>
 A;Cross-references: GB:AE002093; NID:94262240; PIDN:AAD14533.1; GSPDB:GN00139
 C;Genetics:
 A;Map Position: 2

E8/040
 acyl-CoA synthase [imported] - Mycobacterium leprae
 C;Species: Mycobacterium leprae
 C;Accession: E87040
 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho eam, M.A.; Rutherford, K.M.; Devlin, K.; Dutfoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001
 A;Author: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq A;Title: Massive gene decay in the leprosy bacillus.
 A;Reference number: A86909; PMID:21128732; PMID:11234002
 A;Accession: E87040
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-476 <STO>
 A;Cross-references: GB:AL450380; NID:g13093059; PIDN:GAC31432.1; GSPDB:GN00147
 C;Genetics:
 A;Gene: xc1C
 C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
 Query Match 78 .0%; Score 32; DB 2; Length 476;
 Best Local Similarity 57 .1%; Pred. No. 82;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GHRPLDK 7
 Db 271 GHRPLDK 277

Db 1 GHRPLDK 4

RESULT 15
 T17245
 hypothetical protein DKFZp586J0917.1 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T17245
 R;Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
 A;Reference number: Z18722
 A;Accession: T17245
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-878 <KOS>
 A;Cross-references: EMBL:AI117455
 A;Experimental source: adult uterus; clone DKFZp586J0917.1
 C;Genetics:
 A;Note: DKFZp586J0917.1

Query Match 78 .0%; Score 32; DB 2; Length 878;
 Best Local Similarity 71 .4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 403 GHRPLDK 409

RESULT 16
 F70464
 hypothetical protein aq_1912 - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
 C;Accession: F70464
 R;Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; On V.
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; PMID:38196666; PMID:9537320
 A;Accession: F70464
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown.
 A;Molecule type: DNA
 A;Residues: 1-485 <AQF>
 A;Cross-references: GB:AF000763; NID:g2984178; PIDN:ARC07717.1; PMID:92984185; GB:AE00065
 C;Genetics:
 A;Gene: aq_1912

Query Match 78 .0%; Score 32; DB 2; Length 485;
 Best Local Similarity 85 .7%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7

Search completed: June 16, 2003, 16:05:01
 Job time : 13.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2003, 16:00:53 ; Search time 6.06667 Seconds
(without alignments)
47.857 Million cell updates/sec

Title: US-09-424-940A-1
Perfect score: 41
Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	41	100.0	31	1	FIBB_CANFA	P02677 canis familiaris	
2	41	100.0	491	1	FIBB_HUMAN	P02675 homo sapiens	
3	36	87.8	468	1	FIBB_BOVIN	P02676 bos taurus	
4	35	85.4	463	1	FIBB_CHICK	P02620 gallus gallus	
5	35	85.4	479	1	FIBB_RAT	P14480 ratus norvegicus	
6	32	78.0	560	1	FPS_MOUSE	Q64355 mus musculus	
7	32	78.0	1080	1	HDA4_CHICK	P83038 gallus gallus	
8	32	78.0	1084	1	HDA4_HUMAN	P56324 homo sapiens	
9	31	75.6	168	1	MBP_RABBIT	P25274 oryctolagus cuniculus	
10	31	75.6	169	1	MBP_BOVIN	P02687 bos taurus	
11	31	75.6	215	1	PCP_BACSU	P28613 bacillus subtilis	
12	31	75.6	333	1	MRW_ZYMMO	Q8rcq9 zymomonas moryi	
13	31	75.6	363	1	TRMA_PSEFL	Q9rsu9 pseudomonas fluorescens	
14	31	75.6	374	1	TGT_SYN3	Q55983 synechocystis sp	
15	31	75.6	424	1	THC2_METTH	Q27617 methanobacter thermoacetophilus	
16	31	75.6	633	1	IPA2_SHIFL	P18010 shigella flexneri	
17	30	73.2	50	1	INS2_BATSP	P01338 batrachoides inscriptus	
18	30	73.2	184	1	HXB1_AMBME	P31357 ambystoma laterale	
19	30	73.2	231	1	YEDJ_ECOLI	P46144 escherichia coli	
20	30	73.2	253	1	ISPDI_RALSO	Q8xrw3 ralstonia eutropha	
21	30	73.2	269	1	IOD3_RANCA	P49898 ranunculus	
22	30	73.2	285	1	TRUA_PSEAE	Q87016 pseudomonas aeruginosa	
23	30	73.2	334	1	ACOD_PIG	Q02858 sus scrofa	
24	30	73.2	344	1	CD2_MOUSE	P08920 mus musculus	
25	30	73.2	344	1	CD2_RAT	P08211 ratus norvegicus	
26	30	73.2	347	1	CD2_HORSE	P37938 equus caballus	
27	30	73.2	354	1	ACOD_MESEAU	P36420 mesocricetus auratus	
28	30	73.2	355	1	ACOL_MOUSE	P13516 mus musculus	
29	30	73.2	358	1	ACO2_MOUSE	P13011 mus musculus	
30	30	73.2	358	1	ACOD_RAT	P07308 ratus norvegicus	
31	30	73.2	359	1	ACOD_BOVIN	Q9t794 bos taurus	
32	30	73.2	359	1	ACOD_HUMAN	Q60649 homo sapiens	
33	30	73.2	359	1	ACOD_SHEEP	Q82849 ovis aries	

ALIGNMENTS						
RESULT 1						
ID	FIBB_CANFA	STANDARD;	PRT;	31	AA.	
AC	P02677;					
DT	21-JUL-1986	(Rel. 01, Created)				
DT	01-OCT-1989	(Rel. 12, Last sequence update)				
DT	15-JUN-2002	(Rel. 41, Last annotation update)				
DE	Fibrinogen beta chain	[Contains: Fibrinopeptide B] (Fragment).				
GN	FGB.					
OS	Canis familiaris (dog)					
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.					
RN	NCBI_TaxID=9615;					
RN	[1]					
RP	Bloombäck B., Bloombäck M., Grondahl N.J.;					
RT	"Studies on fibrinopeptides from mammals."					
RL	Acta Chem. Scand. 19:1789-1791(1965).					
RN	[2]					
RP	"The location of tyrosine-O-sulphate in fibrinopeptides."					
RT	Acta Chem. Scand. 22:1339-1346(1968).					
RN	[3]					
RX	Medline=6066367; Pubmed=572635;					
RA	Birken S., Wiiner G.D., Canfield R.E.; "Studies of the structure of canine fibrinogen."					
RT	Thromb. Res. 7:599-610(1975).					
RN	[4]					
RP	SEQUENCE OF 1-19.					
RA	Bloombäck B., Bloombäck M., Grondahl N.J.;					
RT	"Studies on fibrinopeptides from mammals."					
RL	Acta Chem. Scand. 19:1789-1791(1965).					
RN	[5]					
RP	SEQUENCE OF 1-19.					
RA	Krajewski T., Bloombäck B.;					
RT	"The location of tyrosine-O-sulphate in fibrinopeptides."					
RL	Acta Chem. Scand. 22:1339-1346(1968).					
CC	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.					
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.					
CC	-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.					
CC	PIR: A03123; A03123; DR: PIR: A03297; DR: InterPro: IPR02187; Fibrinogen_C.					
DR	PROSITE: PS00514; FBIRINAG_C_DOMAIN; PARTIAL.					
KW	Blood coagulation; Plasma; Sulfation.					
FT	PEPTIDE	1	19			
FT	CHAIN	20	>31			
FT	MOD_RES	2	2			
FT	MOD_RES	3	3			
FT	NON_TER	31	31			
SQ	SEQUENCE	31 AA;	3731 MW;	A043727257698156 CRC54;		
	Query Match	100.0%	Score 41;	DB 1;	Length 31;	
	Best Local Similarity	100.0%	Pred. No.	0.018;	Mismatches 0;	
	Matches 7;	Conservative 0;	Indels 0;	Gaps 0;		
Qy	1 GHRPLDK 7					

RESULT 2

Db 20 GHRPLK 26

FIBB_HUMAN ID STANDARD; PRT; 491 AA.

AC P02675; (Rel. 01, Created 21-JUL-1986 (Rel. 26, Last sequence update) DT 01-JUL-1993 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].

GN Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

OX RN

SEQUENCE FROM N.A. MEDLINE=91344740; PubMed=2102623; RX RA Chung D.W., Harris J.E., Davie E.W.; RT "Nucleotide sequences of the three genes coding for human fibrinogen."; RT Adv. Exp. Med. Biol. 281:39-48(1990).

RP SEQUENCE FROM N.A. MEDLINE=93283433; PubMed=6688356; RX RA Chung D.W., Que B.G., Rixon M.W., Macé M. Jr., Davie E.W.; RT "Characterization of complementary deoxyribonucleic acid and genomic deoxyribonucleic acid for the beta chain of human fibrinogen."; RL Biochemistry 22:3244-3255(1983).

RN [3]

RP SEQUENCE FROM N.A. MEDLINE=94030001; PubMed=6688356; RX RA Chung D.W., Harris J.E., Davie E.W.; RT "Nucleotide sequences of the three genes coding for human fibrinogen."; RT (In) Liu C.Y., Chien S. (eds.); RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48, Plenum Press, New York (1991).

RN [4]

RP SEQUENCE FROM N.A., AND VARIANTs SR-100; HIS-170; LEU-265 AND LYS-478. MEDLINE=94030001; PubMed=6688356; RX RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.I., Poel C.L., Yi Q., Nickerson D.A.; RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE. MEDLINE=95124640; PubMed=420779; RX RA Henschel A., Lottspeich F., Southan C., Topfer-Petersen E.; RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural variants."; RL Peeters H. (eds.); RT Protides of the biological fluids, Proc. 28th colloquium, pp.51-56, Pergamon Press, Oxford (1980).

RN [6]

RP SEQUENCE OF 31-491. MEDLINE=95124640; PubMed=420779; RX RA Watt K.W., Takagi T., Doolittle R.F.; RT "Amino acid sequence of the beta chain of human fibrinogen."; RL Biochemistry 18:68-76(1979).

RN [7]

RP SEQUENCE OF 31-148, AND DISULFIDE BONDS. MEDLINE=7625080; PubMed=936108; RX RA Blomback B., Hessel B., Hogg D.; RT "Disulfide bridges in N-terminal part of human fibrinogen."; RL Thromb. Res. 8:639-658(1976).

RN [8]

RP SEQUENCE OF 1-38 FROM N.A. MEDLINE=8714683; PubMed=3029722; RX RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z., Marquerie G.; RT "Characterization of the 5'-flanking region for the human fibrinogen beta gene."; RT Nucleic Acids Res. 15:1615-1625(1987).

[9] RN SEQUENCE OF 31-44. RP PubMed=8915531; RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.; RT "Studies on fibrinopeptides from primates."; RN [10] RT Acta Chem. Scand. 19:1788-1789(1965).

RP AND DISULFIDE BONDS. MEDLINE=83254370; PubMed=6575689; RX RA Fehschen A., Lottspeich F., Kehl M., Southan C.; RT "Covalent structure of fibrinogen."; RL Ann. N.Y. Acad. Sci. 408:28-43(1983).

GN DE FGB. RN [11]

RP DISULFIDE BONDS. MEDLINE=77245999; PubMed=8915531; RX RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blombeck B.; RT "Primary structure of human fibrinogen. Characterization of disulfide-containing cyanogen-bromide fragments."; RL Eur. J. Biochem. 77:595-610(1977).

RN [12]

RP DISULFIDE BONDS. MEDLINE=77245999; PubMed=8915531; RX RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A., Cassman K.C., Goldbaum D.M., Doolittle L.R., Friesner S.J.; RT "The structures of fibrinogen and fibrin."; RL (In) Magnusson S., Ottesen M., Folmann B., Dano K.; RT Neurath H. (eds.); RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172, Pergamon Press, New York (1978).

RN [13] RN [14] RN [15]

RP EM STRUCTURE, POLYMERIZATION, AND LIGANDS. MEDLINE=84305751; PubMed=6383194; RX RA Doolittle R.F.; RT "Fibrinogen and fibrin."; RL Annu. Rev. Biochem. 53:195-229(1984).

RN [16]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491. MEDLINE=97472408; PubMed=9333233; RX RA Reverse S.J., Spraggan G., Doolittle R.F.; RT "Crystal structures of fragment D from human fibrinogen and its crosslinked counterpart from fibrin."; RL Nature 389:455-462(1997).

RN [17]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491. MEDLINE=98923956; PubMed=962875; RX RA Reverse S.J., Spraggan G., Veerapandian L., Riley M., Doolittle R.F.; RT "Crystal structure of fragment double-D from human fibrin with two different bound ligands."; RL Biochemistry 37:8637-8642(1998).

RN [18]

RP X-RAY CRYSTALLOGRAPHY. MEDLINE=99175089; PubMed=10074346; RX RA Reverse S.J., Spraggan G., Veerapandian L., Doolittle R.F.; RT "Conformational changes in fragments D and double-D from human fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide."; RL Biochemistry 38:2941-2946(1999).

RN [19]

RP VARIANT BALTIMORE-2. MEDLINE=89058942; PubMed=3194832; RX RA Schmelzer C.H., Ebert R.F., Bell W.R.; RT "A polymorphism at B beta 448 of fibrinogen identified during structural studies of fibrinogen Baltimore II."; RL Thromb. Res. 52:173-177(1988).

RN [20]

RP VARIANT ISF. MEDLINE=91208408; PubMed=2018836; RX RA Yoshida N., Wada H., Morita K., Matsuda M., Yamazumi K.; RT Asakura S., Shirakawa S.; RT "A new congenital abnormal fibrinogen isf characterized by the replacement of B beta glycine-15 by cysteine."; RL Blood 77:1958-1963(1991).

RN [21]

RP VARIANT NAPLES. MEDLINE=92340664; PubMed=1634610; RX RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.; RA

RT "Molecular basis of fibrinogen Naples associated with defective thrombin binding and thrombophilia. Homozygous substitution of B beta 68 Ala-->Thr.";
 RT J. Clin. Invest. 90:238-244 (1992).
 [20]

RN RP VARIANTS IJNPUTDEN AND NIJMEGEN-N.
 RX MEDLINE:92228809; PubMed:1665641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogen IJnputden (B beta Arg14-->Cys) and Nijmegen (B
 RT beta Arg44-->Cys) form disulfide linked fibrinogen-albumin
 complexes";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 [21]

RN RP VARIANT NEW YORK-1.
 RX MEDLINE:85157605; PubMed:3156856;
 RA Liu C.Y., Kochn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 exon 2 of the gene.";
 RT J. Biol. Chem. 260:4390-4396(1985).
 CC -I- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.

CC -I- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE, DIVERRGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH CONNECT THE CENTRAL NODULE TO THE DISTAL MODULES CONTAINING THE DISPLA DOMAINS, EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL ENDS OF THE ALPHA CHAINS.

CC -I- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.

CC -I- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOGENIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES EPISILON-(GAMMA-(GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT MONOMERS.

CC -I- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collabora
 CC between the Swiss Institute of Bioinformatics and the EMBL outstat
 CC the European Bioinformatics Institute. There are no restrictions on
 CC use by non profit institutions as long as its content is in no
 CC modified and this statement is not removed. Usage by and for commer
 CC entities requires a license agreement. See <http://www.ebi.ac.uk/annotation/>

GN	MBP.	Oryctolagus cuniculus (Rabbit).	Pred. No. 16;
OS		Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	Matches 5; Conservative 1; Mismatches 1;
OC		Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae;	Indels 0; Gaps 0;
OX		NCBI_TAXID=9886;	
RN	[1]		
RP		PRELIMINARY SEQUENCE.	
RC		TISSUE-Sciatic nerve.	
RX		Medline=73190037; PubMed=4662101;	
RA		Brostoff S.W., Eylar E.H.;	
RT		*The proposed amino acid sequence of the P1 protein of rabbit sciatic nerve myelin.";	
RT		RT "Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";	
RN	[2]		
RP		SEQUENCE OF 45-86.	
RA		Shapiro R., McNeilly S.S., Chou F., Kibler R.F.;	
RT		RT "Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";	
RN	[3]		
RP		PHOSPHORYLATION.	
RX		Medline=83108902; PubMed=6185481;	
RA		Martenson R.E., Law M.J., Debler G.E.;	
RT		*Identification of multiple in vivo phosphorylation sites in rabbit myelin basic protein.	
RT		RT "Basic AI protein of the myelin membrane. The complete amino acid sequence."	
RL		J. Biol. Chem. 258:930-937(1983).	
CC	-1-	FUNCTION: Is, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers.	
CC	-1-	Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).	
CC	-1-	SUBCELLULAR LOCATION: Cytoplasmic side of myelin.	
CC	-1-	TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.	
CC	-1-	PRM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	
CC	-1-	PTM: The N-terminus is blocked.	
CC	-1-	SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.	
DR		PTR; B32087; B92087.	
DR		HSSP; P02686; 100%.	
DR		InterPro; IPR00548; Myelin_BP.	
DR		PRINTS; PR00212; MYELINMBP.	
DR		PROSITE; PS00569; MYELIN_MBP; 1.	
KW		Myelin; Structural Protein; Acetylation; Methylation; Phosphorylation; Citrullination; Autoimmune encephalomyelitis.	
KW		INDUCES EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS (EAE).	
FT	MOD_RES	1	ACETYLATION (PROBABLE).
FT	MOD_RES	7	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	25	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	31	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	56	PHOSPHORYLATION.
FT	MOD_RES	96	PHOSPHORYLATION.
FT	MOD_RES	101	DEAMIDATION (PARTIAL) (PROBABLE).
FT	MOD_RES	105	METHYLATION (MONO- OR DI-).
FT	MOD_RES	113	PHOSPHORYLATION.
FT	MOD_RES	128	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	145	DEAMIDATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	157	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	159	PHOSPHORYLATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	163	PHOSPHORYLATION.
FT	MOD_RES	168	CITRULLINATION (BY SIMILARITY).
FT	CONFlict	46	S->G (IN REF. 2).
SQ		SEQUENCE 18217 MW; EC3C97ACD2C08EA6 CRC64;	
Query Match		75.6%; Score 31; DB 1; Length 168;	

"Localization of methylated arginine in the A1 protein from myelin.";
 Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).
 [9]

POST-TRANSLATIONAL MODIFICATIONS.
 MEDLINE# 76167591; PubMed# 57115;

Chou F.C.-H., Chou C.-H.J., Shapira R., Kibler R.F.;
 "Basis of microheterogeneity of myelin basic protein.";
 J. Biol. Chem. 251:2671-2679(1976).
 [10]

SEQUENCE OF 97-104, AND PHOSPHORYLATION OF THR-97.
 MEDLINE# 91060584; PubMed# 1709979;

Erickson A.K., Payne D.M., Martino P.A., Rossinando A.J.,
 Shabanowitz J., Weber M.J., Hunt D.F., Sturgill T.W.;
 "Identification by mass spectrometry of threonine 97 in bovine myelin
 basic protein as a specific phosphorylation site for mitogen-activated
 protein kinase.";
 J. Biol. Chem. 265:19728-19735(1990).
 [11]

POST-TRANSLATIONAL MODIFICATIONS.
 MEDLINE# 98153125; PubMed# 9485392;

Zand R., Li M.X., Jin X., Lubman D.;
 Determination of the sites of posttranslational modifications in the
 charge isomers of bovine myelin basic protein by capillary
 electrophoresis-mass spectroscopy.";
 Biochemistry 37:2441-2449(1998).

DIMERIZATION.
MEDLINE=80198320; PubMed=6155143;
Smith R.;
"Sedimentation analysis of the self-association of bovine myelin basic protein.";
Biochemistry 19:1826-1831(1980).
 - I- FUNCTION: Is, with PIP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).
 - I- SUBUNIT: Homodimer; self-associates in the presence of lysolipid.
 - I- SUBCELLULAR LOCATION: Cyttoplasmic side of myelin.
 - I- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
 - I- PIM: At least 6 charge isomers; C1 (the most cationic and least modified form), C2, C3, C4, C5 AND C6 (the less cationic form);

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to bioinfo@isb-sib.ch.)

ENSLB; AF226693; AAK00645.1;	-		
PPR; A03140; MBBOB.			
HSSP; P02685; 1OCL.			
InterPro; IPR000548; Myelin_BP.			
Pfam; PF016650; Myelin_MBP; 1.			
PRINTS; PRO0212; MYELINMBP.			
PROSITE; PS00569; MYELIN_MBP; 1.			
Myelin; Structural Protein; Acetylation; Methylation; Phosphocitrylination; Autoimmune encephalomyelitis.			
DOMAIN 43 87 INDUCES EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS (EAE). 1.			
DOMAIN 114 122 INDUCES EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS (EAE). 2.			
MOD_RES 1 1 ACETYLATION.			
MOD_RES 7 7 PHOSPHORYLATION (IN C5 AND C6).			

FT	MOD_RES	23	23	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	29	29	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	54	54	PHOSPHORYLATION (IN C4, C5 AND C6).
FT	MOD_RES	97	97	PHOSPHORYLATION (BY MAPK) (IN C3, C4, C5 AND C6).
FT	MOD_RES	102	102	DEAMIDATION (IN C5).
FT	MOD_RES	106	106	METHYLATION (MONO- OR DI-).
FT	MOD_RES	114	114	PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES	129	129	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	146	146	DEAMIDATION (IN C2).
FT	MOD_RES	158	158	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	160	160	PHOSPHORYLATION (IN C4 AND C6).
FT	MOD_RES	164	164	PHOSPHORYLATION (IN C3, C5 AND C6).
FT	MOD_RES	169	169	CITRULLINATION (PROBABLE).
SQ	SEQUENCE	169 AA;	18323 MW;	8E1157B7A1978484 CRG64;
Query Match	Best Local Similarity	75.6%	Score 31; DB 1; Length 169;	
Matches	5;	Conservative	Pred. No. 16;	
			Mismatches 1; Indels 0; Gaps	
Qy	1	GHRPLDK 7		
Db	76	GRHPDQE 82		
RESULT 11				
PCP_BACSU	ID	PCP_BACSU	STANDARD;	PRT;
AC	P28618;			215 AA.
DT	01-DEC-1992	(Rel. 24, Created)		
DT	01-DEC-1992	(Rel. 24, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Pyroglutidone-carboxylate peptidase (EC 3.4.19.3)	(5'-oxoprolyl-peptidase)	(Pyroglutamyl-peptidase I) (PGP-I) (Pyrase).	
GN	PCP			
OS	Bacillus subtilis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TAXID=1423;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=168;			
RX	MEDLINE=92339537; PubMed=1353026;			
RA	Awade A., Cleuziat P., Gonzales T., Robert-Baudouy J.;			
RT	"Characterization of the pcp gene encoding the pyroglutidone carboxyl-peptidase of <i>Bacillus subtilis</i> ."			
RL	FEBS Lett. 305:67-73(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=168;			
RX	MEDLINE=98044033; PubMed=9384377;			
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azzevedo V., Bertier M.G., Bessieres P., Bolotin A., Borchart S., Brönn S., Borriss R., Boursier L., Bräus A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita Y., Fuma S., Galizzi N., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Giuseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaer Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapins A., Lardinois S., Lauber J., Laarvick V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,			
RA	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,			

Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portebeau D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynoids S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Satoh T., Scanlan F., Schleicher S., Schroeber R., Scoffone R., Sekiguchi J., Sekowska A., Seror S.J., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Tahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandembol M., Vannier F., Vassarotti A., Viala A., Wambutt R., Wedler E., Weitznecker T., Winters P., Witap A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A., "the complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*." Nature 390:249-256(1997).

DT	15-JUN-2002	(Rel. 41, Last sequence update)
DT	15-JUN-2002	(Rel. 41, Last annotation update)
DE	S-adenosyl-methyltransferase mraw	(EC 2.1.1.-).
GN	MRAW OR ZM110RF5 OR ZM160RF1.	
OS	Zymomonas mobilis.	
OC	Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;	
OC	Zymomonas.	
NCBI-TAXID	542;	
RN	[1]	
SEQUENCE FROM N.A.		
STRAIN	ATCC 31821 / ZM4 / CP4;	
RC		
RA	Dm H.W., Kang H.S.;	
RU	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.	
CC	-i- FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase activity (BY SIMILARITY).	
CC	-i- SIMILARITY: BELONGS TO THE MRAW FAMILY.	
CC		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC		
DR	EMBL; AF179611; ADD53943; 1; -;	
DR	EMBL; AF213822; AF213886; 1; -;	
DR	InterPro; IPR002903; Bac_Metnfrse.	
CC	Pfam; PF01795; Methyltransf_5; 1.	
DR	Prodrom; PD000685; Bac_Metnfrse; 1.	
DR	TIGRFARS; TIGR00006; UP00117; 1.	
KW	Transferase; Methyltransferase.	
SEQUENCE	333 AA; 37347 MW; A090B25F84587FF79 CRC64;	
Qy	1 GHRPLDK 7	
Db	192 GYRFEDK 198	
RESULT 13		
TRNA_PSEFL		
ID	TRNA_PSEFL	
AC	09RHS9;	
STANDARD		
PRT	363 AA.	
15-JUN-2002 (Rel. 41, Created)		
15-JUN-2002 (Rel. 41, Last sequence update)		
15-JUN-2002 (Rel. 41, Last annotation update)		
DB	RNA (Trac1-5')-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54) - methyltransferase) (RNUTRA).	
GN		
OS	Pseudomonas fluorescens	
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	
OC	Pseudomonas.	
NCBI-TAXID	294;	
RN	[1]	
SEQUENCE FROM N.A.		
STRAIN NO.	33;	
RC		
RX	MedlineB-200636; PubMed-10601212;	
RA	Idei A., Kawai E., Akatsuka H., Omori K.;	
RA	"Cloning and characterization of the Pseudomonas fluorescens ATP-binding cassette exporter, HasDEF, for the heme acquisition protein HasA."	
RP	J. Bacteriol. 181:1545-1551(1999).	
RP	-i- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity).	
CC	-i- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing thymine.	
CC	-i- SIMILARITY: BELONGS TO THE RNA M5U METHYLTRANSFERASE FAMILY. TRNA SUBFAMILY.	

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```

EMBL; AB023289; BAA88495.1; -
InterPro; IPR000051; SAM_bind.
InterPro; IPR01566; tRNA.
PROSITE; PS01230; tRNA_1.
PROSITE; PS01231; tRNA_2; FALSE; NEG.
Transferase; Methyltransferase; tRNA processing.
DOMAIN 213 219 S-ADENOSYLMETHIONINE BINDING (BY SIMILARITY).
ACT-SITE 321 321 BY SIMILARITY.
SEQUENCE 363 AR; 41258 MW; 5B2F53954180AE38 CRC64;
Query Match 75.6% Score 31; DB 1; Length 363;
Best Local Similarity 83.3%; Pred. No. 38; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
2 HRPDLK 7
11111;
127 HRPDLDE 132

```

RESULT 14

TGT_SYN3	STANDARD;	PRT;	374 AA.
055983;			
01-NOV-1997	(Rel. 35, Created)		
01-NOV-1997	(Rel. 35, Last sequence update)		
15-JUN-2002	(Rel. 41, Last annotation update)		
Queuine tRNA-ribosyltransferase (EC 2.4.2.29)	(tRNA-guanine transglycosylase) (Guanine insertion enzyme).		
TGT OR SLR0713			
Synechocystis sp. (strain PCC 6803).			
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.			
[1]			
SEQUENCE FROM N.A.			
MDLNAME=96127529; Published=8530279;			
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiyama M., Tabata S.,			
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 648 to 928 of the genome.";			
DNA Res. 2:153-166 (1995).			
-I- FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7'-deazguanine in tRNAs with GU(N) anticodons (tRNA Asp, -Asn, -His and -Tyr). After the exchange, a cyclopentadienyl moiety is attached to the 7-aminomethyl group of 7-deazguanine, resulting in the hypermodified nucleoside queuosine (Q) (7-((4,5-cis-dihydro-2-cyclopenten-1-yl)amino)methyl)-7-deazguanosine (BY SIMILARITY).			
-I- CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine + guanine.			
-I- COPARTNER: BINDS AND REQUIRES ZINC FOR ACTIVITY. ALSO REQUIRES MAGNESIUM (BY SIMILARITY).			
-I- SIMILARITY: BELONGS TO THE QUEUINE tRNA-RIBOSYLTRANSFERASE FAMILY.			

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```

EMBL; D64005; BAA10764.1; -
HSSP; P28720; IPD.

```

```
Query Match      75.6%; Score 31; DB 1; Length 424;  
Best Local Similarity 71.4%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy      1 GHRPLDK 7  
        || |||:  
Db      267 GHAPLDQ 273
```

Search completed: June 16, 2003, 16:03:34
Job time : 7.06667 secs

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2003, 16:01:29 ; Search time 22.4 Seconds
(without alignments)
64.390 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41 Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20647115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_invertebrate:
 5: sp_mammal:
 6: sp_mhc:
 7: sp_organelle:
 8: sp_phage:
 9: sp_plant:
 10: sp_rabbit:
 11: sp_rat:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_uniclassified:
 15: sp_rvirus:
 16: sp_bacteriaph:
 17: sp_archaea:

ALIGNMENTS

RESULT 1
 Q8WW77 PRELIMINARY;
 ID Q8WW77:
 AC 08WW77:
 DT 01-MAR-2002 (T-TREMBLrel. 20, Created)
 DT 01-MAR-2002 (T-TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (T-TREMBLrel. 21, Last annotation update)
 DE Hypothetical 46.9 kDa protein.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI-TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDJB databases.
 DR EMBL; BC020762; AAH0762.; -
 DR InterPro; IPR002181; Fibrinogen.C.
 DR SMART; SMC0186; FBG; 1.
 DR Pfam; PF00147; Fibrinogen.C; 1.
 DR SMART; SMC0503; G-alpha; 1.
 DR Pfam; PF00503; G-alpha; 1.
 DR KW HYPOTHETICAL PROTEIN; G-protein_alpha.
 SQ SEQUENCE 411 AA; 46884 MW;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	41	100.0	411	4	Q8WW77		Q8ww77 homo sapien
2	37	90.2	923	5	Q9VA50		Q9va50 drosophila
3	36	87.8	201	16	Q92XY9		Q92xy9 rhizobium m
4	36	87.8	471	10	Q8SB40		Q8sb40 oryza sativ
5	36	87.8	735	10	Q94B87		Q94eb87 oryza sativ
6	36	87.8	1490	10	Q9MIC7		Q9mic7 arabidopsis
7	35	85.4	505	4	Q9HA50		Q9ha50 homo sapien
8	35	85.4	959	2	Q46583		Q46583 desulfobivir
9	35	85.4	1371	4	Q9Y2K2		Q9y2k2 homo sapien
10	34	82.9	673	3	Q94ZJ7		Q94zj97 thermoanaer
11	34	82.9	673	3	Q94271		Q94271 schizophacch
12	34	82.9	795	10	Q951Z7		Q951z7 arabidopsis
13	33	80.5	67	9	Q94MM0		Q94mw0 bacterioph
14	33	80.5	225	16	Q9RXW3		Q9rxw3 deinococcus
15	33	80.5	226	16	Q983T8		Q983t8 rhizobium l
16	33	80.5	244	2	Q93JU5		Q93ju5 pseudomonas

RESULT 2
 Q9VA50 PRELIMINARY;

RESULT 2
 Q9VA50 PRELIMINARY;

RESULT 5						
Q94EB7	PRELIMINARY;	PRT;	735	AA.		
AC Q94EB7;						
DT 01-DEC-2001 (TREMBLrel. 19, Created)						
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)						
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)						
DE B1045D11_13. protein.						
GN B1045D11_13.						
OS Oryza sativa (Rice).						
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;						
OC Ehrhartoideae; Oryzeae; Oryza.						
NCBI_TAXID=4530;						
RN [1]						
SEQUENCE FROM N. A.						
RA STRAIN=CV. NIIPPONBARE;						
RA Sasaki T., Matsunoto T., Yamamoto K.;						
RA "Oryza sativa nippobare (Ga3) genomic DNA, chromosome 1, BAC						
RF clone: B1045D11_13.						
RU Submitted (FEB-2001) to the EMBL/GenBank/DDJB databases.						
DR AP003199; BAB6117_1; -						
EMBL; IPR001092; HLH_Basic.						
DR InterPro: IPR002885; PPR.						
DR pfam; PF01535; PPR; 11.						
DR TIGRFARS; TIGR00756; PPR; 7.						
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.						
SEQUENCE 735 AA; 79898 MW; 540392FCBF125EF6 CRC64;						
Query Match 87.83; Score 36; DB 10; Length 735;						
Best Local Similarity 100.0%; Pred. No. 45;						
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gap 0;						
SGQ 1 GHRPLD 6						
11111						
DB 94 GHRPLD 99						
RESULT 6						
Q9M1C7	PRELIMINARY;	PRT;	1490	AA.		
AC Q9M1C7;						
CC 09M1C7;						
DT 01-OCT-2000 (TREMBLrel. 15, Created)						
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)						
DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update)						
DE Multi resistance protein homolog.						
OS Arabidopsis thaliana (Mouse-ear cress).						
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae						
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.						
NCBI_TAXID=3702;						
RN [1]						
RP SEQUENCE FROM N. A.						
RA EU Arabidopsis sequencing project;						
RA Submitted (FEB-2000) to the EMBL/GenBank/DDJB databases.						
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.						
DR EMBL; AL138655; ABT7931_1; -						
DR HSSP; PI3569; 1NB.						
DR InterPro: IPR003593; AAA_ATPase.						
DR InterPro: IPR01140; ABCtransprtM.						
DR InterPro: IPR003439; ABC_transprt.						
PF Pf00664; ABC_membrane; 2.						
PF Pf0005; ABC_tran; 2.						
PRODOM; PD00006; ABC_transportr; 2.						
SMART; SM00382; AAA; 2.						
PROSITE; PS00211; ABC_TRANSPORTER; 1.						

Matches	5;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;		"Two recombination-dependent DNA replication pathways of bacteriophage T4, and their roles in mutagenesis and horizontal gene transfer.";
Qy	1 GHRPLDK 7 :	PRELIMINARY;	PRT;	.795 AA.						RT	Proc. Natl. Acad. Sci. U.S.A. 98:8306-8311(2001).
Db	160 GHHPMDK 166									RL	DR
										SQ	SEQUENCE 67 AA; 8010 MW; D8C5AA794200D0A6 CRC64;
RESULT 12											
Q9S1Z7	PRELIMINARY;	PRT;	.795 AA.								
ID	Q9S1Z7										
AC	Q9S1Z7;										
DT	01-MAY-2000 (TREMBLrel. 13, Created)										
DT	01-JUN-2002 (TREMBLrel. 13, Last sequence update)										
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)										
DE	At2g22020 protein.										
GN	Arabidopsis thaliana (Mouse-ear cress).										
OS	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.										
OC											
OC											
NCBI_TaxID=3702;											
RN	[1]										
RP	SEQUENCE FROM N.A.										
RC	STRAIN=CV. COLOMBIA;										
RX	MEDLINE=20083487; PubMed=10617197;										
RA	Lin X., Kaul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Fieldblyum T.V., Cronin L.A., Keichum K.H., Lee J.J., Ronning C., Koo H., Moffat T.S., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Salzberg S.L., Fraser C.M., Nierman W.C., White O., Eisen J.A., RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).										
RA	[2]										
RN	SEQUENCE FROM N.A.										
RC	STRAIN=CV. COLOMBIA;										
RA	Lin X.;										
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.										
DR	EMBL: AC007019; AAC20419.1; -										
DR	InterPro: IPR003878; SPRY_domain.										
DR	InterPro: IPR003877; SPRY_receptor.										
DR	Pfam: PF00622; SPRY_1.										
DR	SMART: SM00449; SPRY_1.										
DR	SEQUENCE 795 AA; 89006 MW; 07625DE69BBFE0D CRC64;										
Query Match	82.9%; Score 34; DB 10; Length 795;										
Best Local Similarity	71.4%; Pred. No. 1.2e+02;										
Matches	5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;										
Qy	1 GHRPLDK 7 :	PRELIMINARY;	PRT;	.67 AA.						RT	RT
Db	41 GHRPLER 47									RL	PRELIMINARY;
										AC	PRELIMINARY;
RESULT 13										AC	PRELIMINARY;
Q944W0	PRELIMINARY;	PRT;	.67 AA.							AC	PRELIMINARY;
ID	Q944W0									AC	PRELIMINARY;
AC	Q944W0;									AC	PRELIMINARY;
DT	01-DEC-2001 (TREMBLrel. 19, Created)									AC	PRELIMINARY;
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)									AC	PRELIMINARY;
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)									AC	PRELIMINARY;
DE	ORF_soc_2.									AC	PRELIMINARY;
GN	SOC_2.									AC	PRELIMINARY;
OS	Bacteriophage T6.									AC	PRELIMINARY;
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;									AC	PRELIMINARY;
OC	T4-like viruses.									AC	PRELIMINARY;
OC	NCBITaxID=10666;									AC	PRELIMINARY;
OX										AC	PRELIMINARY;
RN	[1]									AC	PRELIMINARY;
RP	SEQUENCE FROM N.A.									AC	PRELIMINARY;
RX	MEDLINE=21353060; PubMed=11459968;									AC	PRELIMINARY;
RA	Mosig G., Gewin J., Ludder A., Colowick N., Yo D.;									AC	PRELIMINARY;
										AC	PRELIMINARY;
RESULT 14											
Q9RXW3	PRELIMINARY;	PRT;	.225 AA.							RT	RT
ID	Q9RXW3									RL	PRELIMINARY;
AC	Q9RXW3;									AC	PRELIMINARY;
DT	01-MAY-2000 (TREMBLrel. 13, Created)									AC	PRELIMINARY;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)									AC	PRELIMINARY;
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)									AC	PRELIMINARY;
DE	MUR/NUDIX family protein.									AC	PRELIMINARY;
GN	Deinococcus radiodurans.									AC	PRELIMINARY;
OC	Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.									AC	PRELIMINARY;
OC										AC	PRELIMINARY;
OC										AC	PRELIMINARY;
OC										AC	PRELIMINARY;
OX	Deinococcus radiodurans R1.									AC	PRELIMINARY;
RN	[1]									AC	PRELIMINARY;
RP	SEQUENCE FROM N.A.									AC	PRELIMINARY;
RC	STRAIN=CV. COLOMBIA;									AC	PRELIMINARY;
RA	Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.L., Richardson D.L., Noffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;									AC	PRELIMINARY;
RA	RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1."; Science 286:1571-1577(1999).									AC	PRELIMINARY;
RA	RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;									AC	PRELIMINARY;
RA	RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.									AC	PRELIMINARY;
DR	DR InterPro: IPR003878; SPRY_domain.									AC	PRELIMINARY;
DR	DR InterPro: IPR003877; SPRY_receptor.									AC	PRELIMINARY;
DR	DR Pfam: PF00622; SPRY_1.									AC	PRELIMINARY;
DR	DR SMART: SM00449; SPRY_1.									AC	PRELIMINARY;
DR	DR SEQUENCE 795 AA; 89006 MW; 07625DE69BBFE0D CRC64;									AC	PRELIMINARY;
Query Match	80.5%; Score 33; DB 16; Length 225;									RT	RT
Best Local Similarity	85.7%; Pred. No. 60;									RL	PRELIMINARY;
Matches	6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;									AC	PRELIMINARY;
Qy	1 GHRPLDK 7 :	PRELIMINARY;	PRT;	.67 AA.						AC	PRELIMINARY;
Db	41 GHRPLER 47									AC	PRELIMINARY;
										AC	PRELIMINARY;
RESULT 15											
Q983T8	PRELIMINARY;	PRT;	.226 AA.							RT	RT
ID	Q983T8									RL	PRELIMINARY;
AC	Q983T8;									AC	PRELIMINARY;
DT	01-OCT-2001 (TREMBLrel. 18, Created)									AC	PRELIMINARY;
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)									AC	PRELIMINARY;
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)									AC	PRELIMINARY;
DE	Probable glutathione S-transferase.									AC	PRELIMINARY;
GN	MUR8180.									AC	PRELIMINARY;
OS	Rhizobium loti (Mesorhizobium loti).									AC	PRELIMINARY;
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;									AC	PRELIMINARY;
OC	Phyllobacteriaceae; Mesorhizobium.									AC	PRELIMINARY;
OX	NCBI_TaxID=381;									AC	PRELIMINARY;
RN	[1]									AC	PRELIMINARY;

RP SEQUENCE FROM N.A.
 STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Ikesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpoo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti."
 RL DNA Res. 7:331-338 (2000).
 DR EMBL: AP003013; BAB53792; 1; -.
 DR Interpro; IPR04045; GST_Nterm.
 DR Pfam: PF02798; GST_N; 1.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 226 AA; 25616 MW; 739465BBDD0F670 CRC64;
 Query Match 80.5%; Score 33; DB 16; Length 226;
 Best Local Similarity 83.3%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GHRPLD 6
 ||:|||
 Db 132 GHKPLD 137

Search completed: June 16, 2003, 16:04:30
 Job time : 25.4 secs


```

; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-4

Query Match          100.0%; Score 41; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.057; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GHRPLDK 7
Db      15 GHRPLDK 21

RESULT 3
US-10-131-543-5
; Sequence 5, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: Synthetic construct
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
; US-10-131-543-5

Query Match          100.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.071; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GHRPLDK 7
Db      15 GHRPLDK 21

RESULT 4
US-10-131-346-5
; Sequence 5, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0

Query Match          100.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.071; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GHRPLDK 7
Db      15 GHRPLDK 21

RESULT 5
US-10-131-546-5
; Sequence 5, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: Synthetic construct
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
; US-10-131-546-5

Query Match          100.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.071; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GHRPLDK 7
Db      15 GHRPLDK 21

RESULT 6
US-10-017-724-6
; Sequence 6, Application US/10017724
; Publication No. US2003009958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: AMI-004
; CURRENT APPLICATION NUMBER: US/10/017-724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16

```

```

| NUMBER OF SEQ ID NOS: 11
| SOFTWARE: FASTSEQ for Windows Version 4.0
| SEQ ID NO: 6
| LENGTH: 491
| TYPE: PRT
| ORGANISM: Homo Sapiens
| OS-10-017-724-6

Query Match      100.0%;  Score 41;  DB 9;  Length 491
Best Local Similarity 100.0%;  Pred. No. 1.7;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0

Qy      1 GHRPLDK 7
Db      45 GHRPLDK 51

RESULT 7
OS-10-142-935-9
Sequence 9, Application US/10142935
Publication No. US20030044418A1
GENERAL INFORMATION
APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING
FILE REFERENCE: P0201US01/BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/290,072
PRIOR FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 9
LENGTH: 10
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
OS-10-142-935-9

Query Match      87.8%;  Score 36;  DB 9;  Length 10
Best Local Similarity 100.0%;  Pred. No. 0.22;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0

Qy      1 GHRPLD 6
Db      5 GHRPLD 10

RESULT 8
OS-10-142-935-8
Sequence 8, Application US/10142935
Publication No. US20030044418A1
GENERAL INFORMATION
APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING
FILE REFERENCE: P0201US01/BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/290,072
PRIOR FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 8
LENGTH: 15
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
OS-10-142-935-8

Query Match      87.8%;  Score 36;  DB 9;  Length 15
Best Local Similarity 100.0%;  Pred. No. 0.35;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0

```

```

; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053 -4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-094-9

Query Match          78.0%;  Score 32;  DB 9;  Length 855;
Best Local Similarity 71.4%;  Pred. No. 2.4e+02;
Matches 5;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;
Qy      1 GHRPLDK 7
Db      437 GHRPLSR 443

RESULT 14
US-09-563-728A-30
; Sequence 30, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-728A-30

Query Match          78.0%;  Score 32;  DB 9;  Length 967;
Best Local Similarity 71.4%;  Pred. No. 2.7e+02;
Matches 5;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;
Qy      1 GHRPLDK 7
Db      506 GHRPLSR 512

RESULT 15
US-09-817-913-7
; Sequence 7, Application US/09817913
; Patent No. US20000081860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zoumei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09817913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,57
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-817-913-13

Query Match          78.0%;  Score 32;  DB 10;  Length 855;
Best Local Similarity 71.4%;  Pred. No. 2.4e+02;
Matches 5;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;
Qy      1 GHRPLDK 7
Db      437 GHRPLSR 443

RESULT 13
US-09-817-538-13
; Sequence 13, Application US/09817538
; Patent No. US2002137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zoumei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/811,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Human
US-09-817-538-7

Query Match          78.0%;  Score 32;  DB 10;  Length 967;
Best Local Similarity 71.4%;  Pred. No. 2.7e+02;
Matches 5;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

```

Qy 1 GHRPLDK 7
 |||||:
Db 506 GHRPLSR 512

Search completed: June 16, 2003, 16:16:36
Job time : 28.5333 secs